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Run
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Perfect score:
                                                             Database
                                                                                                         Post-processing: Minimum Match
Maximum Match
                                                                                                                                                      Minimum DB
Maximum DB
                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                    Searched:
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                                                                                                                                                                                                                                                                                                             Sequence:
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seq length: 2000000000
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649
PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
                                                                                                                                                                                                                               283308 seqs, 96168682 residues
                                                                                                                                                                                                                                                                Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                      February 18,
                                                                                         Listing first 45 summaries
                                                                                                                                                                                                                                                                                                           PLATROGKRPSKNLKARCSR....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                       2004, 17:39:55; Search time 20 Seconds (without alignments) 572.204 Million cell upda
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	00	7	6	5	4	ω	2		Result No.
329	330	330	331	332	333	333	333	337	338	339	341	341	343	343	344	346	346	347	347	347	347	353.5	493	528	543	639	640		Score
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Vg-1-related prote	bone morphogenetic		vgr protein - rat	bone morphogenetic	decapentaplegic pr	bone morphogenetic	bone morphogenetic	morphogeneti	bone morphogenetic	morphogeneti	bone morphogenetic	SPDVR1 protein - s	bone morphogenetic	cartilage-derived	bone morphogenetic	cartilage-derived	bone morphogenetic	owth/different	Description										

# ALIGNMENTS

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C;Accession: S43294
C;Accession: S43294
R;Storm, E.E.; Huynh, T.V.; Copeland, N.G.; Jenkins, N.A.; Kingsley, D.M.; Lee, S.J.
Rature 368, 639-643, 1994
A;Title: Limb alterations in brachypodism mice due to mutations in a new member of the A;Reference number: S43294; MUID:94195427; PMID:8145850
A;Accession: S43294
A;Accession: S43294
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-495 <8TO>
A;Cross-references: GB:U08337; NID:9488461; PIDN:AAA18778.1; PID:9488462
A;Cross-references: GB:U08337; NID:9488461; PIDN:AAA18778.1; PID:9488462
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c;Superfamily: inhibin
C;Keywords: glycoprotein
F;189/Binding site: carbohydrate
F;381-382/Cleavage site: Arg-Ala
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Blochem. Blophys. Res. Commun. 204, 646-652, 1994
A;Title: Cloning and expression of recombinant human growth/differentiation factor A;Reference number: JC2347; MUID:95071375; PMID:7980526
A;Accession: JC2347
A;Molecule type: DNA
A;Residues: 1-501 <HOB>
A;Cross-references: GB:X80915; NID:g671524; PIDN:CAA56874.1; PID:g671525
C;Genetics:
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                                                                                                                                                                                                                                                                                            bone morphogenetic protein-related protein (GDF5) - mouse C;Species: Mus musculus (house mouse) C;Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-2000
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C; Superfamily: inhibin
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99.2%;
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Pred. No. 4.6e-59;
0; Mismatches 1
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Nature 368, 639-643, 1994
A;Title: Limb alterations in brachypodism mice
A:Reference number: S43294; MUID:94195427; PMII
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S43295
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A;Title: Cartilage-derived morphogenetic proteins. New members of the transforming A;Reference number: A55452; MUID:95050604; PMID:7961761
A;Accession: A55452
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Nature 368, 639-643, 1994
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A; Residues: 1-501 < CHA>
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A; Residues: 1-125 < STO>
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;Alternate names: growth and differentiation factor 6
;Species: Mus musculus (house mouse)
                                                                                                                 ;Superfamily: inhibin
;1-5/Domain: polybasi
                                                                                                                                                                                                                                                                                                              ;Species: Homo sapiens (man)
;Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 17-Mar-2000
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                                   Score 543; DB Pred. No. 3.7e
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3.7e-49;
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L.9e-58;
les 2;
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SPDVR1 protein - sea urchin (Strongylocentrotus purpuratus)
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change
                                                 RESULT
S52408
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bone morphogenetic protein-related protein (GDF7) - C;Species: Mus musculus (house mouse) C;Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #C;Accession: S43296 R;Storm, E.E.; Huynh, T.V.; Copeland, N.G.; Jenkins, R;Storm, E.E.; Huynh, T.V.; Copeland, N.G.; Jenkins,
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B55452
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A; Accession: $43296
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C;Superfamily: inhibin
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A; Residues: 1-151 <S
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                                                                                                                                                                                                                                                                                             Nature 368, 639-643, 1994
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Best Local S
Matches 83
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                                                         GRGHGRRGRSRCSRKSLHVDFKELGWDDWIIAPLDYEAYHCEGVCDFPLRSHLEPTNHAI
                                                                                   GKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPTNHAV
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IQTILINSMAPDAAPASCCVPARLSPISILYIDAANNVVXKQYEDMVVEACGCR
                           IQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR
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                                                                                                                                                                                       GB:U08339; NID:g488465; PIDN:AAA18780.1; PID:g488466
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76.9%;
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73.5%;
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Pred. No. 5.4e-47;
.6; Mismatches 11
                                                                                                                Score 493; DB 2;
Pred. No. 7.1e-44;
0; Mismatches 10
                                                                                                                                                                                                                                                                                                                                      10-Nov-1995 #text_change
                                                                                                                                                                                                                                                                                                           Jenkins, N.A.;
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                                                                                                                                                                                                                                                                                                                                                                    mouse
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20~Sep~1999

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C;Accession: S52408
R;Ponce, M.R.; Micol, J.L.; Davidson, E.H.
submitted to the EMBL Data Library, February 1995
A;Description: SpDVR1, a member of the transforming growth factor-beta superfamily expre
                                                                      Biochim. Biophys. Acta 1218, 221-224, 1994
A;Title: Structure and sequence of mouse bone morphogenetic protein-2
A;Reference number: S45355; MUID:94289485; PMID:8018727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:Z25868; NID:g397950; C;Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Feng, J.Q.; Chen, D.; Fer submitted to the EMBL Data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bone morphogenetic protein 2 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Jan-1995 #sequence_revision 06
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                                                                                                                          C;Accession: S45355
R;Feng, J.Q.; Harris, M.A.; Ghosh-Choudhury, N.;
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A; Residues: 1-393 < FEN>
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A; Reference number: S37073
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                                                        A; Accession: S45355
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                                                                                                                                                                                                     bone morphogenetic protein-2 - mouse
;Molecule type: DNA;Residues: 1-394 <FEN:
                                 Status: preliminary
                                                                                                                                                               ;Species: Mus musculus (house mouse);Date: 10-Dec-1994 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AFHCEGLCEFPLRSHLEPTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNV
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                                                                                                                                                                                                                                                                                                                                                                        ROAKHKORKRIKSSCKRHPLYVDFSDVGWNDWIVAPPGYHAFYCHGECPFPLADHINSTN
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                                                                                                                                                                                                                                                                                                  HAIVQTLVNSVN-SKIPKACCVPTELSAISMLYLDENEKVVLKNYQDMVVEGCGCR
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48.1%;
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54.3%;
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se of fetal rat calvaria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 347; DB 2;
Pred. No. 2.9e-28
7; Mismatches 3
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Pred. No. 7.3
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                                                                                                                                                              17-Nov-1995 #text_change
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nes 32;
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                                                                                                                          Feng, M.; Mundy, G.R.; Harris,
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F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-265/Domain: propeptide #status predicted <PRO>
F;266-396/Product: bone morphogenetic protein 2, long form #status predicted <MP
F;283-396/Product: bone morphogenetic protein 2 #status predicted <MP
F;283-396/Product: bone morphogenetic protein 2 #status predicted <MP
F;283-396/Product: bone morphogenetic protein 2 #status predicted contains the protein of the protein contains predicted f;283-396/Product: bone morphogenetic protein 2 #status predicted contains pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: cell line BoMo-15AIIc R; Rathore, S.; Hammerstone, K.M.; Dansereau,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: protein
A;Residues: 290-295,'X',297-304 <ISH>
A;Experimental source: cell line BoMo
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C; Keywords: bone; dimer; glycoprotein; pyroglutamic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein Sci. 4 (Suppl.2), 443S, A; Title: N-terminal isoforms o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-396 < WO2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz, Science 242, 1528-1534, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bone morphogenetic protein 2 precursor - human N;Alternate names: bone morphogenetic protein 2A; rhBMP2
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Date: 16-Sep-1992 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
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                                                             64 HAVIOTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
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Pred. No. 2.9e-28;
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Pred. No. 2.9e-28;
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bone morphogenetic protein 4 precursor - African clawed frog C;Species: Xenopus laevis (African clawed frog) C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999 C;Accession: JH0689
C;Accession: JH0689
C;Nishimatsu, S.; Suzuki, A.; Shoda, A.; Murakami, K.; Ueno, N.
Biochem. Biophys. Res. Commun. 186, 1487-1495, 1992
A;Title: Genes for bone morphogenetic proteins are differentially transcribed in early A;Reference number: JH0687; MUID:92378616; PMID:1510675
A;Rocession: JH0687; MUID:92378616; PMID:1510675
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C; Superfamily: in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N;Alternate names: C;Species: Xenopus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: XTC
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Pred. No. 3.8e-28;
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Pred. No. 3e-28;
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RESULT
JH0688
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A;Gene: FlyBase:dpp
A;Gene: FlyBase:FlyBase:FBgn0000490
C;Keywords: glycoprotein
F;1-15/Domain: signal sequence #status predicted <SIG>
F;120,342,377,529/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Drosophila melanogaster
C;Date: 24-Jun-1987 #sequence_revision 24-Jun-1987
C;Accession: A26158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C;Accession: I50608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Padgett, R.W.; St
Nature 325, 81-84,
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                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:M30116; NID:g157291;
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                               A;Residues:
                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             decapentaplegic protein precursor -
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A; Residues: 1-405 < FRA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Bone morphogenetic proteins and a signalling pathway A;Reference number: I50607; MUID:94163974; PMID:8119128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Francis, P.H.; Richardson, M.K.; Brickell, P.M.; Tickle, Development 120, 209-218, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bone morphogenetic protein 4 - chi
C;Species: Gallus gallus (chicken)
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                                                                                                                                                                                                                                                                                                                                                                               1-588 <PAD>
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                                   NHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR
NHAVVOTEVNIMNPGKVPKACCVPTOLDSVAMLYLNDQSTVVLKNYQEMTVVGCGCR
                                                                               RHARRPTRRKNHDDTCRRHSLYVDFSDVGWDDWIVAPLGYDAYYCHGKCPFPLADHFNST
                                                                                                                  RQGKRPS--KNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPT 62
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48.7%;
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52.1%;
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Pred. No. 9.3e-28;
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Pred. No. 3.8e-28;
1; Mismatches 31;
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A;Experimental source: occyte (;Superfamily: inhibin C;Superfamily: inhibin C;Keywords: glycoprotein C;Keywords: glycoprotein E;285-398/Product: bone morphogenetic protein 2II #status predicted <MAT> F;285-398/Product: bone morphogenetic protein (Asn) (covalent) #status predicted F;137,202,237,340/Binding site: carbohydrate (Asn) (covalent)
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A;Molecule type: mRNA
A;Residues: 1-398 <NIS>
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Search completed: February 18, 2004, 17:43:53 Job time : 21 secs
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                                                                                                                                                                                                                                              Query Match 52.9%; Score 343; DB 2; Length 39
Best Local Similarity 53.4%; Pred. No. 7.6e-28;
Matches 62; Conservative 19; Mismatches 33; Indels
                                                                                                                                                           344 HAIVQTLVNSVN-TNIPKACCVPTELSAISMLYLDENEKVVLKNYQDMVVEGCGCR 398
                                                                                                      64 HAVIQTIMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
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Result
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Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
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     Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Match
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     SwissProt_41:*
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     GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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UNIV STRPU
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UNIV STRPU
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                                                                    046564 oryctolagus
019006 dama dama (
P12643 homo sapien
p30885 xenopus lae
p91706 drosophila
090752 gallus gallus
P25703 xenopus lae
p25703 xenopus lae
p21275 mus musculu
006826 rattus norv
P12644 homo sapien
0226974 tribolium c
029607 dama dama (
090751 gallus gallus
93110 gallus
p3110 gallus
p31693 mus musculu
046576 oryctolagus
p35621 brachydanio
p91699 trattus norv
p49003 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                         P43026 homo sapien
P43027 mus musculu
P43028 mus musculu
P55106 bos taurus
P43029 mus musculu
P43029 strongyloce
P48970 strongyloce
P48970 strongyloce
P48970 strongyloce
P48970 strongyloce
       P22003
P22004
P18075
P20722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
       homo sapien
homo sapien
homo sapien
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RESULT 1 GDF5_HUMAN GDF5_GDF5_		45	44	43	42	41	40	9	38	37	36	35	34	
LT 1 HUMAN GDF5 HUMAN		291.5	293.5	297.5	300.5	302	303	304	313	314.5	317.5	327	328	
		44.9	45.2	45.8	46.3	46.5	46.7	46.8	48.2	48.5	48.9	50,4	50.5	
STANDARD;		364	428	420	424	436	427	455	360	399	402	430	426	
		ب	۳	1-4	<b>1</b> -1	-	۲	ب	μ.	<u>_</u>	1-	μ	٢	
PRT; 501 AA.	ALIGNMENTS	GDF3_HUMAN	GDF2_MOUSE	BM10 MOUSE	BM10_HUMAN	60A DROVI	DSL1_CHICK	60A DROME	DVR1 XENLA	BM8A MOUSE	BMPB_HUMAN	BMP7_MOUSE	BMP7_XENLA	
		Califas Homo septem	-				P34822 Gantagart							

RA RA	RA R	RA RA	<b>R</b> 3	2 R 3	2 R	RA.	R A	R.A	R R	RA	RA RA	R.A	문문	RN	RI.	7 P.	RT	RA	₩ X	RC RC	RP.	Z Z	점점	RA	<b>R</b> ?	989	R O	88	88	GN CN CN CN CN CN CN CN CN CN CN CN CN CN	D E	D I			RESULT
e C.D., Smith M.L n R.M., Sycamore	B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Si	D., Moore M.J.F., Mullikin J.C., Nickels I., Patel R., Pearce T.A.V., Peck A.I.,	Martin S.L., McConnach	Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,	Hammond S., Harley J.L., Heath F.D., HO S., Nother C.M., Johnson D.,	Il R.E	יי	Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.K.,	Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,	geman A.M.,	eard L.M., Beare D.M.,	. i			J. Biol. Chem. 269:28227-28234 (1994).		"Cartilage-derived morphogenetic proteins. New members of the	.H., Moos M.;	ر. در د	οн	SEQUENCE FROM N.A.	Biochem. Biophys. Res. Commun. 204:646-652(1994). [2]	Gaston of recommens	, Neidha	7980526;	SEQUENCE FROM N.A.	NCBI_TaxID=9606;	ia; Primates; Catarrhini; Hominidae; Homo.	Chordata:	GDES OR CDMP1.	wth/differe	(Rel. 42, Last annotation update)	(Rel. 32, Creat	ڌ	I T. I

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RA Strausberg R.L., Peingold E.A., Grouse I.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shaemen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Donaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., McDevan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Pahey J., Helton E., Ketteman M., Macan A., Rodrigues S., Sanchez A.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smallus D.E.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Skalaka U., Smallus D.E.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Skalaka U., Smallus D.E.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Skalaka U., Smallus D.E.,
RA Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA Scherch S. S. Schemat
                                                                                                                                                                                                                                                                                                                                      PIR; A55452; A55452.

PIR; JC3347; JC2347.

HSSP; P12643; 3BMP.

Genew; HGNC:4220; GDF5.

MIM; 601146;
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"The DNA sequence and connature 414:865-871(2001)
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  Probom; PD000357; ...
Probom; PD000357; ...
SMART; SM00204; TGFB; 1.
SMART; PS00250; TGF BETA 1; 1.
Correct Problems: Cytokine;
                                                                               GO; GO:000083; F:growth factor activity; TAS.
GO; GO:0005515; F:protein binding activity; TAS.
GO; GO:0007517; P:cell-cell signaling; TAS.
GO; GO:0007179; P:TGFbeta receptor signaling pathway;
InterPro; IPR001839; TGFb.
InterPro; IPR001839; TGFb.
Pfam; PF00018; TGFb-beta; I.
Pfam; PF00018; TGFb-beta; I.
Pfam; PF00018; TGFb propeptide; 1.
Prodon; PD000357; TGFb; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RADIUS IS CURVED AND ITS HEAD IS OFTEN DISLOCATED POSTERIORLY. THE METACARDALS, METATARSALS AND PHALANGES ARE PARTICULARLY SHORT. THE PHALANGES ARE ALMOST SQUARE.
SIMILARITY: Belongs to the TGF-beta family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      U13660; AAA57007.1; -. AL121586; CAB89416.1; BC032495; AAH32495.1;
Tromans A.C., Vaudin M., Wall M., Wallis
S.L., Whittaker P., Willey D.L., Williams
, Wray P.W., Hubbard T., Durbin R.M., Bent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA57007.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comparative analysis of human chromosome 20.";
                          Glycoprotein; Dwarfism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    llis J.M.,
iams L., Williams S.
Bentley D.R., Beck
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RESULT
GDF5_MC
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CARBOHYD
CONFLICT
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HSSP; P12643; 3MMP:
MGD; MGI:95688; Gdf5.
MGD; MGI:95688; Gdf5.
InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb N.
Pfam; PF00019; TGF-beta; T.
Pfam; PF00688; TGFb_propeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDF5 MOUSE STANDARD; PRT; 495 AA.
P43027;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Growth/differentiation factor 5 precursor (GDF-5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                            "Limb alterations in brachypodism mice due member of the TGF beta-superfamily."; Nature 368:639-643(1994).
                                                                                                                                                                                                                                                                                                                            STRAIN=CD-1; TISSUE=Embryo;
MEDLINE=94195427; PubMed=8145850.
Storm E.E., Huynh T.V., Copeland
                                                                                                                                                                                                                                                                                                                                                                                         NCBI
                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                -!- FUNCTION: COULD BE INVOLVED IN BONE FORMATION.
-!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
-!- DISEASE: DEFECTS IN GDF5 ARE THE CAUSE OF BRACHYPODISM WHICH ALTERS THE LENGTH AND NUMBERS OF BONES IN THE LIMBS BUT SPARES THE AXIAL SKELETON.
                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                        GDF5 OR GDF-5 OR BP
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria;
                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                  Lee S.-J
                                                                     EMBL; U08337; AAA18778.1; PIR; S43294; S43294.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         383
                                                                                                                                                                                                                                                                                                                                                                                           TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR
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T -> S (IN REF. 2).
APGGG -> VPRSR (IN REF. 2).
S -> A (IN REF. 2).
A -> T (IN REF. 2).
L -> S (IN REF. 2).
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BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi;
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MBL outstation -
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TGF-beta; 1.
TGFb\_propeptide;

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ALD SOON BENGARAN AND SOON BENGARAN BEN
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Signal; G
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                            "Limb alterations in brachypodism mice member of the TGF beta-superfamily."; Nature 368:639-642(1994)
-i- SUBUNIT: Homodimer; disulfide-linke
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P43028;
                                                                                                                                                                                                                             the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                           EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=94195427;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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01-NOV-1995 (Rel.
16-OCT-2001 (Rel.
                 PRINTS; PR00438; GFCYSKNOT.
PRINTS; PR00669; INHIBINA.
ProDom; PD000357; TGFb; 1.
                                                                  InterPro; IPR002400; GF cysknot.
InterPro; IPR002405; Inhibin_alpha.
InterPro; IPR001839; TGFb.
InterPro; IPR001839; TGFb.
Pfam; PF00019; TGF-beta; 1.
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                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Belongs to the TGF-beta family.
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                                                                                                                                          MGI:95689; Gdf6.
                                                                                                                                                                              S43295; S43295.
                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produ
sen the Swiss Institute of Bioinformatics
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TGPB; 1.
TGP BETA
TG CYTC
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E.E., Huynh T.V., Copeland
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                                                                                                                                                             P12643; 3BMP.
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Sciurognathi; Muridae;
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RESULT 4
GDF6_BOVIN
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D55106,

01-OCT-1996 (Rel. 34, Created)

01-OCT-1996 (Rel. 34, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

Growth/differentiation factor 6 precursor (GDF-6)

Growth/differentiation factor 6 precursor (GDF-6)

Growth/differentiation factor 6 precursor (GDF-6)
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                   InterPro; IPR002400; GF cysknot.
InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb.N.
Pfam; PF00019; TGF-beta; I.
Pfam; PF00688; TGFb propeptide; 1
Pfam; PF00688; TGFb propeptide; 1
PRINTS; PR00438; GFCYSKNOT.
PrODOm; PD000357; TGFb; 1.
SMART; SM00204; TGFB; 1.
PROSITE; P800250; TGF BETA_1; 1.
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Chang S., Hoang B., Thomas J.T., Vukicevic S., Luyten F.P.,

Ryba N.J.P., Kozak C.A., Reddi A.H., Moos M.;

Ryba N.J.P., Kozak C.A., Reddi A.H., Moos M.;

"Cartilage-derived morphogenetic proteins. New members of the

transforming growth factor-beta superfamily predominantly expr

in long bones during human embryonic development.";

J. Biol. Chem. 269:28227-28234(1994)

-:- SUBUNIT: Homodimer; disulfide-linked (By similarity).

-:- SUMILARITY: Belongs to the TGF-beta family.
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Mammalia; Eutheria;
Bovidae; Bovinae; B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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B55452; B55452.
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                                                                                                                                                                                                                                                                                                                                                    non-profit instituend this statement requires a license
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Cytokine; Glycoprotein.
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GROWTH/DIFFERENTIATION FACTY
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CARBOHYD
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                                                                                   PROSITE; FU-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Limb alterations in brachypodism mice member of the TGF beta-superfamily."; Nature 368:639-643(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-BALB/c; TISSUE=Liver;
MEDLINE=94105427; PubMedd=8145850;
Storm E.E., Huynh T.V., Copeland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
MCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995
01-NOV-1995
                           NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).-!- SIMILARITY: Belongs to the TGF-beta family.
                                                                                                     PRINTS; PRO0438; GFCYSKNOT.

ProDom; PD000357; TGFb; 1.

SMART; SM00204; TGFB; 1.

PROSITE; PS00250; TGF_BETA_1; 1.

PROSITE; PS00250; TGF_BETA_1; 1.

PROM_MED
                                                                                                                                                                                                                                                         InterPro; IPR002400; GF cysknot.
InterPro; IPR001839; TGFb.
Pfam; PF00019; TGF-beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lee S.-J
DISULFID
                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:95690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                               S43296; S43296.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 U08339; AAA18780.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    w
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(Rel. 32, Last sequence update)
(Rel. 40, Last annotation update)
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76.9%;
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Pred.
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Sciurognathi; Muridae; Murinae; Mus
POTENTIAL.
GROWTH/DIFFERENTIATION FACTOR
BY SIMILARITY.
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No. 3.6e-49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jenkins N.A., Kingsley D.M.
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PROSITE; ***

Twth factor;
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01-FEB-1996 (Rel.
16-OCT-2001 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ponce M.R., Micol J.L., Davidson E.H.;
Submilted (FEB-1995) to the EMBL/GenBank/DDBJ databases
SUBUNIT: HOMODIMER, DISTLIFIDE-LINKED (PROBABLE).
-!- SIMILARITY: Belongs to the TGF-beta family.
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NCBI_TaxID=7668;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restrained to the succession of the success
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HSSP; P18075; 1BMP.
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                                                                                                                                                                                                                                                                                                                           InterPro; IPR002405; Inhib
InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities
                                                                                                                                                                                                                SMART; SM00204; TGFB; 1
PROSITE; PS00250; TGF_BETA
                                                                                                                                                                                                                                                    ProDom; PD000357; TGFb; 1.
                                                                                                                                                                                                                                                                      Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide;
PRINTS; PR00669; INHIBINA.
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; Echinodermata; Eleutherozoa;
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73.5%;
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POTENTIAL
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N-LINKED (GLCNAC. . .) (POTH
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Pred. No. 5.9e-46;
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HSSP; P12643; 3BMP.
InterPro; IPR0018139; TGFb.
InterPro; IPR001111; TGFb.
Pfam; PF00019; TGP-beta; 1.
Pfam; PF00688; TGPb propeptide; 1
ProDom; PD000357; TGFb; 1.
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MEDLINE-95046897; PubMed-7958442;
Stenzel P., Angerer L.M., Smith B.J.,
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NCBI_TaxID=7668;
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                                                                                                                                                                                                                                            entities requires a license agreement or send an email to license@isb-sib.cl
                                                                                                                                                                                                                                                                             modified and this statement is not removed
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                                                                   Prodom; PD000357; TGFL
SMART; SM00204; TGFB;
PROSITE; PS00250; TGF_
                                  SIGNAL
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                                                                                                                                                                                                                                                                                             ween the Swiss Institute of Bioinformatics Institute. The European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: HOMODIMER; DISULFIDE-LINKED (PROBABLE).

DEVELOPMENTAL STAGE: HIGHEST LEVELS OF EXPRESSION IN THE EGG AND PREHATCHING BLASTULA. DURING LATE CLEAVAGE STAGES, IT ACCUMULATES PROGRESSIVELY TO A CIRCUMEQUATORIAL BAND. DURING GASTRULATION IT IS DETECTED PRIMARILY IN THE PRESUMPTIVE POREGUT AND CILIATED
                                                                                                                                                                                                                                                                                                                                                                                 BAND. BY PLUTEUS STAGE, IT IS DETECTED ONLY IN THESE CELL TYPES SIMILARITY: Belongs to the TGF-beta family.
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CT-2000) to the EMBL/GenBank/DDBJ databases
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a; Echinoida; Strongylocentrotidae;
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                                                   Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

TISSUE-Bone;
Feng J.Q., Chen D., Feng M., Harris M.A., Mundy
Submitted (SEP-1993) to the EMBL/GenBank/DDBJ de
-!- FUNCTION: INDUCES CARTILAGE AND BONE FORMAT:
-!- SUBUNIT: Homodimer; disulfide-linked.
-!- TISSUE SPECIFICITY: FEMUR, CALVARIA, TRACHE:
-!- SIMILARITY: Belongs to the TGF-beta family.
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                                                                                    Signal;
                                                                                                              Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb propeptide;
PRINTS; PR00669; INHIBINA.
ProDom; PD000357; TGFb; 1.
SMART; SM00204; TGFB; 1.
PROSITE; PS00250; TGF BETA_1; 1
                                                                                                                                                                                                                                         EMBL; Z25868; CAA81088.1;
PIR; S37073; S37073.
HSSP; P12643; 3BMP.
                                                                                                                                                                                                                                                                                                entities requires a license agreement (or send an email to license@isb-sib.ch)
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Mammalia; Eutheria;
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InterPro; IPR001839; TGFb.
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N-LINKED (GLCNAC. . .) (POT)
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2 precursos
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             BONE MORPHOGENE
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   precursor
                                                                                      ine; Bone; POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; l
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OFA3340DF5A6360E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        352;
                                                          MORPHOGENETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     n update)
or (BMP-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         393
                                                                                                                                                                                                                                                                                                                 (See http://www.isb-sib.ch/announce/
                                                                                                   Cartilage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
?.5e-30;
    (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                              TRACHEA,
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                                                                                                     Glycoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                            restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                  AND
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EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                  OVARY
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RESULT 9
BMP2_MOUSE
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Best Local S
Matches 63
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P21274;
01-MAY-1991
01-FEB-1996
16-OCT-2001
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=94289485; PubMed=8018727;
Feng J.Q., Harris M.A., Ghosh-Choudhury N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bone morphogenetic BMP2 OR BMP-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jenkins N.A.;

Jenkins N.A.;

"Chromosomal localization of seven chromosomal localization c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dickinson M.E., Kobrin M.S., Silan C.M., K Miller D.A., Ceci J.D., Lock L.F., Lee A., Siracusa L.D., Lyons K.M., Derynck R., Hog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=90228966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-351 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochim.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Structure and sequence of (BMP-2): comparison of the and BMP-4 genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Feng J.Q., H
Harris S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no rest
                                                                                                                                                 EMBL; L25602;
PIR; A34201; F
                                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMAT
-!- SUBUNIT: Homodimer; disulfide-linked.
-!- SIMILARITY: Belongs to the TGF-beta family.
                                                                                                                                                                                                                                                                                                                                                                                                                       Genomics 6:505-520(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       339
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63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .A., Cect ...
L.D., Lyons K.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biophys. Acta 1218:221-224(1994).
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393
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(Rel. 33, Last sequence update)
(Rel. 40, Last annotation updat)
genetic protein 2 precursor (BMP)
                                                                                                                                                 A34201.
                                                                                                                                                                                                                                                                Bioinformatics Institute. The profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                 INDUCES CARTILAGE AND BONE Homodimer; disulfide-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA,
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44383 .
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Rodentia;
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M); 7DZ0865852E0F213 CRC64;
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structures
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nnotation update)
precursor (BMP-2)
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Pred. No. 8
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Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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several
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           morphogenetic and promoter r
                                                                                                                                                                                                                         noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A., Buchberg A.M.,
Hogan B.L.M., Cop
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.7e-30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             morphogenetic mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the murine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copeland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mundy G.R.,
                                                                                                                                                                                                                                                                                    he EMBL outstation restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Justice M.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0fi
                                                                                                                                                                                                                                                                                                                            a collaboration
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STRIPTION OF THE PROPERTY OF T
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            A PRESENTATION OF THE PROPERTY OF THE PROPERTY
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Best Local S
Matches 63
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SMART; SM00204; TGFB; 1.
PROSITE; PS00250; TGF BETA 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal; Growth
                                 EMBL; AF041421; AAB967
HSSP; P12643; 3BMP.
InterPro; IPR002405; I
InterPro; IPR001839; I
InterPro; IPR001111; I
                                                                                                                                                                                                                                                                                                                                                                                                                              BMP2 RABIT STANDARD;
046564;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last seq
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RABIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BMP2 Or bwr-a.
Oryctolagus cuniculus (Rabbit).
Oryctolagus cuniculus (Rabbit).
Oryctolagus cuniculus (Rabbit).
Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                          use by non-profit institutions as lon modified and this statement is not remove entitles requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bone morphogenetic BMP2 OR BMP-2.
                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=New
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Sears J., Chen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 factor;
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S., Sears M.;
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Pred. No. 8.7e-30;
7; Mismatches 34
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                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restitute the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bone morphogenetic
                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                           "Bone morphogenetic
                                                                                                                                                                                                                                                                                                                                                                                              Harris S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                    HSSP;
                                                                                                                                                                                                                                                                                    FUNCTION: INDUCES CA
SUBUNIT: Homodimer;
                                                                                                                                                                                                                                                                   SIMILARITY: Belongs to the TGF-beta family.
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                                                                  AJ001817; CAA
P12643; 3BMP.
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24 281 EY
282 395 EY
295 360 EY
190 324 392 EY
191 328 394 IN
191 134 N-
191 139 N-
193 337 337 N-
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PR00669; INHIBINA.
PD000357; TGFb; 1.
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., Ghosh-Choudhury
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                                                                                                                     license agreement (S. license@isb-sib.ch).
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(GLCNAC...)
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(See http://www.isb-sib.ch/announce/
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PROSITE; PS00250; TGF_BETA.
Signal; Growth factor; Cyti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRODESS; IGFb_propeptide; PRINTS; PRODESS; INHIBINA. ProDom; PD000357; TGFb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                              HUMAN
Deloukas P., Matthews I.H., Ashurst J., Burton J., Gilbert J.G.
Jones M., Stavrides G., Almedda J.P., Babbage A.K., Bagguley C.
Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.
Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.
Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee
Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.
Graffam D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall
Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden
                                                                                                                                               Submitted [3]
                                                                                                                                                                                                                                                                                                                                                                                                                    BMP2
                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1989
15-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                              P12643;
01-OCT-1989
                                                                                                                                                           Shore B.M., Xu M.-Q., Calvert G., Moriatis J., "Human bone morphogenetic protein 2 (BMP-2) ger Submitted (DEC-1997) to the EMBL/GenBank/DDBJ c
                                                                                                                                                                                                                 activities.";
Science 242:1
                                                                                                                                                                                                                                     MEDLINE-89072730; PubMed=3201241;
Wozney J.M., Rosen V., Celeste A.J.,
Kriz R.W., Hewick R.M., Wang E.A.;
"Novel regulators of bone formation:
                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                    BMP2 OR
                                                                                                                        MEDLINE=21638749;
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                                                                                                                                                                                                                                                                                                                                                             morphogenetic
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                                                                                                                                                                                                                                    regulators
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(Rel. 42, Last annotation
genetic protein 2 precurson
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Pred.
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Catarrhini;
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No. 8.
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(GLCNAC...)
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.8e-30;
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(POTENTIAL)
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pfam; PF00019; TGF-beta; 1
Pfam; PF00688; TGFb propeptide; 1
PRINTS; PR00669; INHIBINA.
ProDom; PD000357; TGFb; 1
SMART; SM00204; TGFB; 1
PROSITE; PS00250; TGF_BETA_1; 1.
                                                                                                                                                                                       PROSITE; PS00:
Signal; Growth
3D-structure.
CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    resolution.";
J. Mol. Biol. 287:103-115(1999).
J. Mol. Biol. 287:103-115(1999).
I. FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
I. SUBUNIT: Homodimer; disulfide-linked.
II LUNG, SPLEEN AND COLON AND IN LOW BUT SIGNIFICANT LEVELS IN HEART, BRAIN, PLACENTA, LIVER, SKELETAL MUSCLE, KIDNEY, PANCREAS, PROSTATE, OVARY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S., Lehvaeslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D., Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A., Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T., Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I., Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H., Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S., Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E., Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., Tracey A., Tromans A.C., Vaudin M., Wall M., Walliams L., Williams S.A., Williams S.A., Williams S.A., Williams S.A., Williams S.A., Williams S.A., Hubbard T., Durbin R.M., Bentley D.R., Beck S...
                                                                      DISULFID CARBOHYD
                                                                                                                DISULFID DISULFID
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                                                                                                                                                                                                                                                                                                       InterPro; IPR002405; Inhibin_alpha.
InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb_N.
                                                                                                                                                                                                                                                                                                                                                   GO; GO:0007267; P:cell-cell signaling; TAS. GO; GO:0001501; P:skeletal development; TAS
                                                                                                                                                                                                                                                                                                                                                                                                             PDB; 3BMP; 12-MAR-00.
PDB; 1ES7; 07-OCT-00.
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                                                            CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The DNA sequence and comparative analysis of human chromosome 20."; Nature 414:865-871(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIVER, SKELETAL MUSCLE, KIDNEY, PANCREAS, E SMALL INTESTINE.
SIMILARITY: Belongs to the TGF-beta family.
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B37278; BMHU2.
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                                                                                                                                                                                                      Growth factor;
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 BETA_1; 1.
Cytokine; Bone; Cartilage;
                           INTERCHAIN.
N-LINKED (G)
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N-LINKED (G)
N-LINKED (G)
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                                                                                                                                                PROTEIN
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RESULT 13
BMP4 XENLA
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Best Local S
Matches 63
                                                                                                                     "DVR-4 (bone morphogenetic protein-4) as a posteri factor in Kenopus mesoderm induction.";
Development 115:639-647(1992)
-i- FUNCTION: POSTERIOR-VENTRALIZING FACTOR IN XEN INDUCTION: INDUCTION SOSTEROVENTRAL MESODERM AND DORSALIZING SIGNALS SUCH AS ACTIVIN.

DORSALIZING SIGNALS SUCH AS ACTIVIN-
-i- SUBUNIT: Homodimer; disulfide-linked (By simil-
-i- SUBCELLULAR LOCATION: SECRETED INTO THE EXTRAC-
-i- SIMILARITY: Belongs to the TGF-beta family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P30885;
01-JUL-1993 (Rel. :
01-JUL-1993 (Rel. :
16-OCT-2001 (Rel. :
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                    between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
entities requires a license agreement (See
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                              Biochem.
                                                                                                                                                                                                                                                                                                      Nishimatsu S., Suzuki A., Shoda A., Mur "Genes for bone morphogenetic proteins in early amphibian embryos.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                    BMP-4 OR DVR-4.
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                                                                                                                                                                                                                                        MEDLINE=93048825; PubMed=1425343; Jones C.M., Lyons K.M., Lapan P.M.,
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Kenopus laevis (African clawed frog).
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                                                                                                                                                                                                                                                                                                                                               MEDLINE=92378616; PubMed=1510675;
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                                                                                   SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
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Pred. No. 8.8e-30;
7; Mismatches 34
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  (See http://www.isb-sib.ch/announce/
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posterior-ventralizing
                                                                                                                                         EXTRACELLULAR MATRIX
                                                                                                                                                      similarity)
                                                                                                                                                                            XENOPUS MESODERM
AND COUNTERACTS
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EMBL; X63426;

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Matches 63
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InterPro; IPRO0111; TGFb N.
Pfam; PF00019; TGF- beta; I.
Pfam; PF00018; TGF- propeptide
ProDom; PD000357; TGFb; 1.
SMART; SM00204; TGFB; 1.
PROSITE; PS00250; TGF BETA 1;
Signal; Growth factor; Cytokir
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                                                                                                                                                   "Molecular evolution at the decapentaplegic locus Genetics 145:297-309(1997).
-!- FUNCTION: ACTS AS AN EXTRACELLULAR MORPHOGEN T
                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                        15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequenc
15-DEC-1998 (Rel. 37, Last annotat
Decapentaplegic protein precursor
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                         Eukaryota;
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                                                                                                                                                                                                                                                           STRAIN-NET
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                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Cuevas M., Gelbart W.M.,
TWO CELLULAR RESPONSE THRESHOLDS WITHIN THE DORSAL HALF OF THE DROSOPHILA MERYO. REQUIRED FOR THE PROPER EVELOPMENT OF THE EMBRYONIC DORSAL HYPODERM, FOR VILABILITY OF LARVAE AND FOR CELL VIABILITY OF THE EPITHELIAL CELLS IN THE IMAGINAL DISKS. ACTS TOGETHER WITH SCW (BY SIMILARITY).

SUBUNIT: HETERODIMERS OF SCW/DDP ARE THE ACTIVE SUBUNIT, DEP/DP HOMODIMERS ELICIT A BASAL RESPONSE AND SCW/SCW HOMODIMERS ALONE ARE INSPECTIVE IN SPECIFYING A DORSAL PATTERN (BY SIMILARITY).
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52.1%;
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BY SIMILARITY.

BONE MORPHOGENETIC PROTEIN 4

BY SIMILARITY.

10 DOI:

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N-LINKED (GLCNAC...) (POTE
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                                                                                                                                                                                                                     Findley S.D.,
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RESULT 15
BMP4_CHICK
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                                                                      STRAIN=White leghorn;
MEDLINE=94163974; PubMed=8119128;
Francis P.H., Richardson M.K., Br
                                                                                                                                                                                                                                                                    BMP4
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DISULFID
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between
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Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                        Bone
                                                        "Bone
                                                                                                              STRAIN=White
                                                                                                                                    SEQUENCE
                                                                                                                                                                                                          Archosauria;
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InterPro; IPR001111; TGFb N.
Pfam; PF00019; TGF-beta; I
Pfam; PF00688; TGFb_propeptide;
                                                                                                                                                                    NCBI_TaxID=9031;
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PROSITE; PS00250; TGF_BETA
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                                                                                                                                                                                                                                                                    OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: Belongs to the TGF-beta family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WITH ESTABLISHMENT OF THE PROXIMAL-DISTAL AND MIDGUT MESODERM (BY SIMILARITY).
                                                                                                                                                                                                                                                                morphogenetic OR BMP-4.
        morphogenetic proteins and a signalling rning in the developing chick limb."; opment 120:209-218(1994).
                                                                                                                                                                                                                                                                                                                                                                                  CHICK
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Pred. No. 1.4e
24; Mismatches
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BY SIMILARITY.
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INTERCHAIN (BY SIMILARITY).
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InterPro; IPR001111; TGFb N.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb propertide; 1
ProDom; PD000357; TGFb; 1.
SMART; SM00204; TGFB; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Development 126:883-894(1999).
-!- FUNCTION: NEGATIVELY REGULATES THE STRUCTURE AND FUNCTION
-!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
-!- SIMILARITY: Belongs to the TGF-beta family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "BMPs negatively regulate structure and function of the limb apical ectodermal ridge.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99128179; PubMed=9927590;
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                                                                                       405
                                                                                                                                   119 R 119
                                                                                                                                                                    346 LNSTNHAIVOTLVNSVN-SSIPKACCVPTELSAISMLYLDEYDKVVLKNYQEMVVEGCGC
                                                                                                                                                                                                                                                            59 LEPTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVBSCGC 118
                                                                                                                                                                                                                                                                                                               4
                                                                                       R 405
                                                                                                                                                                                                                                                                                 TRQGKRP-----SKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSH
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                                                                                                                                                                                                                                                                                                                                                                               53.3%;
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                                                                                                                                                                                                                                                                                                                                                        21;
                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.

BY SIMILARITY.

BONE MORPHOGENETIC PROTEIN 4

BY SIMILARITY.

INTERCHAIN (BY SIMILARITY).

N-LINKED (GLCNAC. . .) (POTEN

N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                     Score 346; DB
Pred. No. 1.2e-
21; Mismatches
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..2e-29;
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Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
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        SPTREMBL 23:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
10: sp_phage:*
10: sp_phage:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_archeap:*
17: sp_archeap:*
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Gapop 10.0 , Gapext 0.5
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649
1 PLATROGKRPSKNI
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sp_mhc:*
sp_organelle:*
sp_phage:*
sp_plant:*
sp_virus:*
sp_virus:*
sp_urclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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56.2	56.4	56.7		59.5	75.7	75.7	80.7	80.7	81.2	0 H	י ר ו ר	82.4	86.7	90.4	98.2	98.6	Match Length	Query	₩
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		09xz69 trippenstes	096504 branchiosto	099mv1 mus muscul	O9bdw8 cerconithec		brachvda	xencous		Q9w6c0 brachydanio	U93573 galling gall		ילטפיזל			O8brw9 mus musculu	Description		

RESULT 2

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QBjij4 steatocranu	081117 1111 idochrom	OBjiko cvorichromi		OBiae3 stichopus i	O8mwq4 patella vul	057574 brachydanio	090723 gallus gall	gallus	026468 schistocerc	acropora mi	013108 brachvdanio	Ogova senonia tro	Ε.,	xenopus la	073818 xenopus lae	Ogvace drosophila	Th.	Xenopus tr	093369 brachvdanio	057573 brachvdanio	2 lammetra :		hemicen	iunonia	x5 rattus no		Q9xyq7 lytechinus	O9xvq8 strongvloce

# ALIGNMENTS

Db Db	ори Ве Ма	RESULT RESULT ACCORDED TO DO	
N) 1-1	Query Match 98.6%; Score 640; DB 11; Length 249; Best Local Similarity 98.3%; Pred. No. 1.7e-67; Matches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0; 1 PLATRQCKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAPHCEGLCEFPLRSHLE 60	M9  QBBRW9  QBBRW9  QBBRW9  QBBRW9  Ol-MAR-2003 (TrEMBLrel. 23, Created)  Ol-MAR-2003 (TrEMBLrel. 23, Last sequence update)  Ol-MAR-2003 (TrEMBLrel. 23, Last sequence update)  Ol-MAR-2003 (TrEMBLrel. 23, Last annotation update)  Growth differentiation factor 5 (Fragment).  Mus musculus (Mouse).  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  Mammalla; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  EUCINE [TaxID=10090;  [1] TaxID=10090;  [1] TaxID=10090;  [1] TaxID=20354683; PubMed=12466851;  The FANTOM Consortium,  the RIKEN Genome Exploration Research Group Phase I & II Team;  "Analysis of the mouse transcriptome based on functional annotation of 80,770 full-length cDMAs.";  Nature 420:563-573(2002).  EMBL; AR041168; BAC30847.1;  NON TER  SEQUENCE 249 AA; 28409 MW; E6EA047F06B57189 CRC64;	

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RESULT CONTROL OF CONT
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ID Q9W6G0
AC Q96G0;
DT Q1-NOV-
DT Q1-NOV-
DT Q1-NOV-
DT Q1-WAR-
DE GDF-5 p
GN GDF5.
OS Gallus
OC Archasa
OC Archasa
OC Archasa
OC Archasa
OC Archas
II
RP SEQUEN(
RX MEDLINI
RA Francis
RA Ladher
RT "Mechar
RL Develoy
CC -1-SIN
DR HSSP;
DR InterP:
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99146893; PubMed=10021348; Francis-West P.H., Abdelfattah A., Chen P., Allen Ladher R., Allen S., MacDherson S., Luyten F.P., I "Mechanisms of GDF-5 action during skeletal development 126:1305-1315(1999).

--- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
EMBL; AF123389; AAD30451.1; ---
EMBL; AF123389; AAD30451.1; ---
EMBL; AF123389; AAD30451.1; ---
EMBL; AF123389; TGFD-5.

InterPro; IPR002405; GF-Cysknot.
InterPro; IPR002405; Inhibin_alpha.
InterPro; IPR001839; TGFb.

InterPro; IPR0011839; TGFb N.

Defam. DEFAD. TGFP-5.--------
INTEROPORTINE TGFP-5.
                                MEDLINE=99119368; PubMed=9918693; Merino R., Macias D., Ganan Y., Economide Stahl N., Sampath K.T., Varona P., Hurle "Expression and function of Gdf-5 during embryonic chick leg bud."; Dev. Biol. 206:33-45(1999).
                                                                                                                                                                                                                                                                                                                                                    01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 20, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Growth differentiation factor 5 (Fragment).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1999 (Tr
01-MAR-2003 (Tr
GDF-5 protein.
                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                Archosauria; Aves; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD000357; TGFb; 1.

SMART; SM00204; TGFB; 1.

PROSITE; PS00250; TGF BETA 1; 1.

SEQUENCE 500 AA; 55952 MW; 1DE8385A3119A598 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001111; TGFb N.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGF-beta; propeptide;
PRINTS; PR00438; GFCYSKNOT
PRINTS; PR00669; INHIBINA.
                                                                                                                                                                                                                                                                                     NCBI_TaxID=9031;
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Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9W6G0;
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                              SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98.2%;
ilarity 97.5%;
Conservative
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  AAD14568.1;
                        BELONGS TO THE
                                                                                                                                                                                                                                                                                                                                   Neognathae;
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                                                                                                                                                                                                                                                                                                                           Chordata; Craniata; Vertebrata; Euteleostomi;
Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12,
12,
23,
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                        TGF-BETA FAMILY
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P., Hurle J.M.;
-5 during digit s)
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cen F.P., Archer
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                                                                                       skeletogenesis
                                                                                                                                         Wang
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Best Local S
Matches 98
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InterPro; IPRO0139; TGFb.
InterPro; IPRO01111; TGFb N.
Pfam; PF00019; TGF-beta; I.
Pfam; PF00688; TGFb propeptide; 1
PFRINTS; PR00669; INHIBINA.
ProDom; PR0069; INTIBINA.
SMART; SM00204; TGFB; 1.
SMART; SM00204; TGFB; 1.
                                                                                                                                                                                            PRINTS; PR0043B; GFCYSKNOT.
PRINTS; PR00669; INHIBINA.
ProDom; PD000357; TGFb; 1.
SMART; SM00204; TGFB; 1.
SMO204; TGFB; 1.
PROSITE; P800250; TGF BETA_1;
                                                                                                                                                                                                                                                                                                       InterPro; IPR002405; Inhibin alpha.
InterPro; IPR001839; TGFb.
Pfam; PF00019; TGF-beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97398455; PubMed=9256353; Bruneau S., Mourrain P., Rosa F.M.; "Expression of contact, a new zebrafish cell lineages in the developing pectoral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   042303
042303;
                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cell lineages in the developing pectoral regulated by retinoic acid.";
Mech. Dev. 65:163-173(1997).
                                                                                                                                                                                   NON TER
                                                                                                                                                                                                                                                                                                                                                                         ZFIN; ZDB-GENE-990415-39; gdf5.
InterPro; IPR002400; GF_cysknot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact
                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brachydanio rerio (Zebrafish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1998
01-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00250; TGF BETA_1;
NON TER 1 1 1
NON TER 324 324
SEQUENCE 324 AA; 37206 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P12643; 3BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                    Y12005; CAA72733.1; -. P12643; 3BMP.
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QGKRPSKNLKARCSRKALHVNFKDMGWDWIIAPLEYBAFHCEGLCBFPLRSHLBPTNHA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLATROCKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAYHCEGLCEFPLRSHLE
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                                                                                                                                     140
257
                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Trambliel.
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                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     324
; 37206 MW;
                                                                                                                                   29787 MW;
                                                                      86.7%;
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97.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23,
                                               10;
                                               Score 563; DB
Pred. No. 2.3e
10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                          POTENTIAL.
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Pred. No. 4.3e-61;
2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata;
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                                                                                                                                   6D64F0542F948849 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGF-BETA FAMILY
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                                        DB 13;
2.3e-58;
6;
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l fins and head
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                                                                                      Length
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RESULT 5
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DT 01-NOV-
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GN GDF6/7
OS Gallus
OC Archosa
OC Archosa
OC Gallus.
Ta RM [1]
RP SEQUEN(
RX MEDLINI
RA Lee K.
RT "Neuror
RT Genes I
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Best Local
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InterPro; IPR002405; Inhibin_alpha.
InterPro; IPR001839; TGFb.
Pfam; PF00019; TGF-beta; 1.
PRINTS; PR00438; GFCYSKNOT.
PRINTS; PR00669; INHIBINA.
ProDom; PD000357; TGFb; 1.
                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation updat
Growth/differentiation factor 7 (Fragment).
                                                                                                                                                                                                                                                      GDF7
               SEQUENCE FROM N.A. MEDLINE=99148135;
                                                                                                   NCBI_TaxID=7955;
                                                                                                                                                                                                                     Brachydanio
                                                                                                                                                                                                                                                                                                                                                                                                Q9W6C0;
                                                                                                                                                                                                                                                                                                                                                                                                                        Q9W6C0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO 1
EMBL; AF089086; AAC97113.1;
HSSP; P12643; 3BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99026113; PubMed=9808626;
Lee K.J., Mendelsohn M., Jessell T.M.;
"Neuronal patterning by BMPs: a requirement for
of a discrete class of commissural interneurons
cord.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00250; TGF_BETA_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genes Dev. 12:3394-3407(1998).
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Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-OCT-2002 (TrEMBLrel. 22, Last annotation update) Putative growth/differentiation factor 6/7 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               093573;
01-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   u; PD000357; TGF
SM00204; TGFB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LATROGKR-PSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTNHAIIQTLMNSMDPESTPPSCCVPSKLSPISILYIDSGNNVVYKQYEDMVVETCGCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTNEAVIQTIMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVYKQYEDMVVESCGCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 AA;
                                                                                                                                                                                                                     rerio (Zebrafish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 08, (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel.
               PubMed=10022976;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14265 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THE TGF-BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 534.5; | Pred. No. 2.4e | 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                               (Danio rerio)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CB824D280F44A394 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                  261
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                                                                                                                                                                                    Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .4e-55;
.es 11;
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                                                                                                                                                   Cypriniformes;
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RESULT POPOSITATION OF PRICE P
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Query Match
Best Local S
Matches 95
HSSF; F12043; Janua.
InterPro; IPR001839; TGFb.
InterPro; IPR001839; TGFb N.
InterPro; IPR001811; TGFb N.
Pfam; PF00019; TGF-beta; T.
Pfam; PF00019; TGFb_propeptide; 1
PRINTS; PR00438; GFCYSKNOT.
ProDom; PD000357; TGFb; 1.
SMART; SM00204; TGFB; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; Pr00019; TGP-beta; 1.
PRINTS; PR00438; GFCYSKNOT.
PRINTS; PR00669; INHIBINA.
PRODom; PD000357; TGFb; 1.
SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9DGN4;
01-MAR-2001
01-MAR-2001
01-MAR-2003
                                                                                                                                                                 epibranchial placodes.",
Mech. Dev. 95:279-282(2000).
-!- SIMILARITY: BELONGS TO THE
EMBL; AF239676; AAF99597.1; -.
                                                                                                                                                                                                                                Vokes S.A., Kriey ....., "Gdf16, a novel member of the "Gdf16, a novel member family,
                                                                                                                                                    EMBL; AF239676; AAI
HSSP; P12643; 3BMP
                                                                                                                                                                                                                              of the TGF-beta superfamily,
                                                                                                                                                                                                                                                                                                                                                             Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Ven
Amphibia; Batrachia; Anura; Mesobatrachia;
                                                                                                                                                                                                                                                                MEDLINE=20368184; PubMed=10906478; 
Vokes S.A., Krieg P.A.;
                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                               Growth/differentiation
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                   Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Powridson A.J., Postlethwait J.H., Yan Y.L., Beier D.R., Foernzler D., Celeste A.J., Crosier K.E., Crosier P.S., "Isolation of zebrafish gdf7 and comparative genetic may belonging to the Growth/Differentiation factor 5, 6, 7 gre-beta superfamily."; Genome Res. 9:121-129(1999).

-!-SIMILARITY: BELONGS TO THE TGF-BETA FAMILY. EMBL, AF113023, AAD20829.1; -.

EMBL, AF113023, AAD20829.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002400; GF cysknot.
InterPro; IPR002405; Inhibin_alpha.
InterPro; IPR001839; TGFb.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS00250; TGF_BETA_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     261 AA; 29414 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                         (TremBirel. 16, Created)
(TremBirel. 16, Last sequence update)
(TremBirel. 23, Last annotation update)
erentiation factor 16 precursor protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                              Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
                                                                                                                                                                                                                                e growth/differentiation is expressed in the hind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 527.5; DB 1
Pred. No. 3.7e-54;
.1; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                  TGF-BETA FAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            413
                                                                                                                                                                                                                                                                                                                                                                         Vertebrata; Euteleostomi;
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protein.
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                                                                                                                                                                                                                                            factor subgroup
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7 subgroup
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  261;
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of the
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RESULT 9
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ID 0129
AC 0129
DT 01-J
DT 01-J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002405; GF cysknot.
InterPro; IPR002405; Inhibin_alpha.
InterPro; IPR001839; TGFb N.
InterPro; IPR001111; TGFb N.
InterPro; IPR001111; TGFb N.
InterPro; IPR001111; TGFb N.
InterPro; IPR001111; TGFb N.
InterPro; IPR00111; TGFb N.
InterPro; IPR00111; TGFb Dropeptide; 1.
InterPro; IPR0068; TGFb Dropeptide; 1.
InterPro; INTERPRO; INTERNA.
INTERPROSE PR00438; GFCTSKNOT.
INTERPROSE PR00669; INHIBINA.
INTERPROSE PR00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 92
               012938;
012938;
01-JUL-1997
01-JUL-1997
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chang C., Hemmati-Brivanlou A.; "Xenopus GDF6, a new antagonist of noggin and a Development 126:3347-3357(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel, 12, 01-NOV-1999 (TrEMBLrel, 12, 01-MAR-2003 (TrEMBLrel, 23, Growth and differentiation f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata
Amphibia; Batrachia; Anura;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9W753;
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chang C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal.
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                                                                                                                                                                                                                                                                            344
                                                                                                                                                                                                                                                                                                                                                                                               284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      355
                                                                                                                                                                                                                                                                                                                                      64
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                                                                                                                                                                                                                                                            HAIIQTIMNISHNIPGSTEPSCCVPTKLTFISILYIDAGNNVVYKQYEDMVVESCGCR
                                                                                                                                                                                                                                                                                                       HAVIQTLMNSMDPESTEPTACVPTRLSPISILFIDSANNVVKQYEDMVVESCGCR
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               (TrEMBLrel.
                                       (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80.7%;
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46510 MW;
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Last
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Pred. No. 1.6e-53;
5; Mismatches 11
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No. 7
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.3e-54;
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RESULT
Q9BDW9
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Best Local S
Matches 88
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Q9BDW9; 17. Crea
01-JUN-2001 (TrEMBLrel. 17, Last
01-JUN-2001 (TrEMBLrel. 23, Last
01-MAR-2003 (TrEMBLrel. 23, Last
Growth/differentiation factor 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002400; GF vysknot.
InterPro; IPR002405; Inhibin alpha.
InterPro; IPR001839; TGpb.
InterPro; IPR001111; TGpb N.
Pfam; PF00019; TGF-beta; I.
Pfam; PF00689; TGF-byropeptide; 1.
PRINTS; PR00448; GFCYSKNOT.
PRINTS; PR00669; INHIBINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Signal.
SIGNAL
CHAIN
                                                            primary motor area of the monkey neocortex."; J. Neurochem. 76:1455-1464(2001).
                                                                                                TISSUE=Cerebral cortex motor area;
MEDLINE=21136583; PubMed=11238730;
Watakabe A., Fujita H., Hayashi M., Yamamori T.;
"Growth/differentiation factor 7 is preferentially
                                                                                                                                                                                                                                                 Macaca fascicularis (Grab eating macaque) (Gynomolgus monkey).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY. EMBL; AF254567; AAK27794.1; -. HSSP; P12643; 3BMP.
                                                                                                                                                                     SEQUENCE FROM N.A. TISSUE=Cerebral co
                                                                                                                                                                                                                               NCBI_TaxID=9541;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata, Actinopterygii; Neopterygii; Cyprinidae; Danio.
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MEDLINE=97231294;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
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SM00204; TGFB; 1.
; PS00250; TGF_BETA_
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a new Zebrafish DVR member
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THAIIQTLMNSNMPSNMPSSCCVPSKLSPISILYIDAGNNVVYKQYEDMVVESCGCR
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412 AA;
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RITY: BELONGS TO THE
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DYNAMO PROTEIN.
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Mammalia; Eutheri;
Cercopithecinae;
NCBI_TaxID=9534;
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SEQUENCE
          CAW66D
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InterPro; IPR001111; TGFb N.
Pfam; PF00019; TGF-beta; I.
Pfam; PF00688; TGFb propeptide;
ProDom; PD000357; TGFb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TremBLrel. 22, 01-OCT-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Watakabe A., Fujita H., Hayashi M., Yamamori T., "Growth/differentiation factor 7 is preferentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDILINE=21136583; PubMed=11238730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDF7.
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ProDom; PD000357; TGFb; 1.
SMART; SM00204; TGFB; 1.
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NON_TER 1 1
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m; PD000357; TGRD; __
l'; SM00204; TGFB; 1.
ITE; PS0025; TGF BETA 1; 1.
447 AA; 45866 MW; DF
                                                                                                                                                    335
                                                                                     395
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                                                                                                                                                                                                                  83;
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                                                                                                                                                           GKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPTNHAV
                                                                                                           IQTIMNSMDESTEPTACVPTRISPISILFIDSANNVVYKQYEDMVVESCGCR 119
                                                                                IQTLLNSMAPDAAPASCCVPARLSPISILYIDAANNVVYKQYEDMVVEACGCR
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IPR001839;
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ilarity 73.5%;
Conservative 1
      PRELIMINARY;
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73.5%;
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TGFb.
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Pred. No. 1.5e-
19; Mismatches
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Pred. No. 9e-5
19; Mismatches
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-I- SIMILARITY: BELONGS TO THE TGF-BETA FA
EMBL; AF254571; AAK30843.1; --
EMBL; AF254570; AAK30843.1; JOINED.
HSSP; P12643; JSMP.
InterPro; IPR0012405; Inhibin_alpha.
InterPro; IPR0012405; TGFb.
InterPro; IPR001111; TGFb.
InterPro; IPR001111; TGFb.
InterPro; IPR001111; TGFb.
Pfam; PF00688; TGFb Dropeptide; 1.
Pfam; PF00688; TGFb Dropeptide; 1.
PFAINTS; PR00669; INHIBINA.
PRINTS; PR00669; INHIBINA.
PRINTS; PR00669; INHIBINA.
ProDom; PD000357; TGFb; 1.
SMART; SM00204; TGFB; 1.
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Best Local
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01-MAY-1999
01-MAY-1999
01-OCT-2002
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SEQUENCE
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01-JUN-2001
01-JUN-2001
01-OCT-2002
                                                                     SEQUENCE FROM N.A.

MEDILINE=98401944; PubMed=9733108;

MEDILINE=98401944; PubMed=9733108;

Menopoulou G.D., Clark M.D., Holland L.Z., Lehrach H.,

"AmphiBMP2/4, an amphioxus bone morphogenetic protein
to Drosophila decapentaplegic and vertebrate BMP2 and
into evolution of dorsoventral axis specification.";

Dev. Dyn. 213:130-139(1998).
                                                                                                                                                                                                                                                          Branchiostoma floridae (Floric
Branchiostoma floridae (Floric
Branchiostoma floridae)
                         EMBL; AF068750;
HSSP; P12643; 31
                                        -!- SIMILARITY: BELONGS TO :
EMBL; AF068750; AAC97488.1;
                                                                                                                                                                                                                       Branchiostoma.
NCBI_TaxID=7739;
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NON_TER 441 441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDF7.
Mus musculus (Mouse)
     InterPro;
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Mammalia; Eutheria;
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     IPR002405;
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441 AA;
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(TrEMBLrel. 10, Last
(TrEMBLrel. 22, Last
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                          3BMP
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Inhibin_alpha
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ordata; Cephalochordata; Branch
                                                    or.
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Pred. No. 3.9e-37;
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                                                           TGF-BETA
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annotation
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                                                                                                               BMP4:
                                                                                                                                                Holland
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NHAVIQTIMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVBSCGCR

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QSZZEGOT 10
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Best Local S
Matches 64
                                                                                                        Matches
                                                                                                                            Query Match
Best Local :
                                                                                                                                                                                                                                                             InterPro; IPR002400; GF cysknot.
InterPro; IPR002405; Inhibin_alpha.
InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb N.
Pfam; PF00019; TGF-beta; I.
Pfam; PF00686; TGFb propeptide; 1.
PFAMT; PF00438; GFCTSKNOT.
PRINTS; PR00439; GFCTSKNOT.
PRINTS; PR00459; INTIBINA.
ProDom; PD000357; TGFb; 1.
SWART; SM00204; TGFB; 1.
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Pfam; PF00619; TGF-beta; 1.
Pfam; PF00688; TGFb propeptide; 1
PRINTS; PR00669; INHIBINA.
PRODOm; PD000357; TGFb; 1.
SMART; SM00204; TGFB; 1.
PROSITE; PS00250; TGF BETA 1; 1.
SEQUENCE 361 AA; 41517 WW; 09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-99262121; PubMed=10329409; Hwang S.L., Chen C.A., Chen C.; "Sea urchin TgBMP2/4 gene encoding a bone morphogenetic closely related to vertebrate BMP2 and BMP4 with maximal the later stages of embryonic development."; Biochem. Biophys. Res. Commun. 258:457-463(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BMP2/4.
Tripneustes gratilla (Hawaian sea urchin).
Tupneustes gratilla (Hawaian sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Eukaryota; Metazoa; Echinacea; Temnopleuroida; Toxopn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Bone morphogenetic protein 2/4 homolog (Fragment).
                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF133305; AAD30538.1;
                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=7673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9XZ69;
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            88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P12643; 3BMP.
                                                         w
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                                                                                                        63;
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                                                                                                                            Similarity
                                            ATROGKRPSKNIKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGICEFPLRSHLEPT
                                                                                                                                                                                                                                       PS00250; TGF_BETA_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
SSRSRKRKGKRLKANCRRHPLYVDFSDVHWNDWIVAPAGYQAYYCHGECPFPLAEHLNTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LATRQ-----GKRPSKNIKARCSRKALHVNFKDMGWDDWITAPLEYEAFHCEGLCEFPLR
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                                                                                                                                                                                                  204 AA;
                                                                                                      Conservative
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                                                                                                                                                                                               23697 MW;
                                                                                                                       56.7%;
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                                                                                                   19;
                                                                                              Score 368; DB
Pred. No. 2.2e
19; Mismatches
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                                                                                                                                                                                             CE829BDC2AA9F077 CRC64;
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2.2e-35;
1es 35;
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                                                                                                                                        Length 204;
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RESULT 15
Q9U41
AC Q9U41
AC Q9U41
AC Q9U41
DT 01-W2
DT 01-W2
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DT 01-W2
CC Branc
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RT Wasui
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Best Local
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HSSP, P12643; 3BMP.
InterPro; IPR002405; Inhibin_alpha
InterPro; IPR001839; TGFb.
InterPro; IPR00111; TGFb N.
Pfam; PF00019; TGF-beta; I.
Pfam; PF00688; TGFb propeptide; 1
PRINTS; PR00669; INHIBINA.
PRODOM; PR000357; TGFb; 1.
SMART; SM00204; TGFB; 1.
PROSITE; PS00250; TGF BETA_1; 1.
SEQUENCE 411 AA; 46929 MW; F5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9U418
Q9U418;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Yasui K., Saiga H., Uemura M., Semba I.;
"Early body formation and expression pattern of genes encodin secreted proteins, BDBMP2/4, BbMnt7, and BbWnt8 in lancelets. Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Branchiostoma belcheri (Amphoxius)
Eukaryota; Metazoa; Chordata; Ceph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-CCT-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=7741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Branchiostoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bone morphogenetic
                      completed: February 18,
                                                                                                             35
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36 secs
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                                                                                                                                                                                                                                                                                                                          l Similarity 62; Conserv
                                                                                               NHAVIQTIMNSMDPESTPPTACVPTRISPISILFIDSANNVVYKQYEDMVVESCGCR
                                                                                                                                                                                                                                   ATROGKRESKNIKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPT
                                                                                                                                                                                                             ANGRKKHQRRRLKANCRRHSLYVDFSDVGWNDWIVAPPGYQAYYCHGECPFPLADHLNST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NHAIVQTLVNSVNPALVPKACCVPTELSAISMLYLDEYEKVVLKNYQDMVVEGCGCR
                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                           56.4%;
53.0%;
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                         2004,
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Pred. No. 8.3e
23; Mismatches
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3.3e-35;
les 32;
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                                                                                                                                                                                                                                                                                                                                                                    Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                             CRC64;
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Title:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                           A_Geneseq_19Jun03;*
1: /SIDS1/gcgdata/g
2: /SIDS1/gcgdata/g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BLOSUM62
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649
1 PLATROGKRPSKNIKARCSR.....ANNVVYKQYEDMVVESCGCR 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gapop 10.0 , Gapext 0.5
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1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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(without alignments)
472.212 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

99.4 501 16	99.4 401 14	99.4 120 24	99.4 120 22	99.4 120 18	99.4	99.4 119 18	99.4 119 17		RESULT Query NO. Score Match Length DB ID	
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New TGF-beta famil	TGF-beta-like Glov	TOTOLOGY PIDE ORIMA	Human MP-52 protei	Himan MDEO protein	rine protein MBE	Human bone inducin	man MP52 growth	Mutant himan WES?	Description	

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í	יני	98	760	16	221	29	9	659	873	659	73	298	86	603	193	σ N	AAB02819	AAB09553	AAY92034	AAR95635	AAM51932	AAY70758	AAY70757	AAY70756	AAY70752	ABG76018	AAB84550	AAR60022	AAB70529	AAW33008	AAW44868	AAW12770	AAW01799	AAW11900	AAW19210	AAW36100
white actd seducity	ייר הייד הייד	10:4454 0			Human growth/Alffe		full	on and	matu		Murine MV2 protein			Himan chart C-term	Murine TGEbeta pro	CDMD-1 /CDF-5 fines		Human CDMP-1/GDR-5	n growth diff	Cartilage-derived	י ע			Methionine oxidise	ביווידר דר דד מדדד	Women cross agreed	-	۲.	TOBE SOFT MO	n Maro	TGF-bets superfine		М О О О О О	high mol w	コロゴープロナッ フィ	Human MP52 Homo

## ALIGNMENTS

PA	XX PR	X F X	dd	ΧX	¥ Ş	H H	×	S	SO	ŠŠ	KW	¥	Ş	Ä	Χį	J X	DT	×	AC.	Χij	RESULT
(HMRI ) HOECHST MARION ROUSSEL LTD.	22-MAY-1998; 98UP-0141379.	14-MAY-1999; 99WO-IB00866.	02-DEC-1999.	WO9961611-A1.	<pre>/note= "Wild-type Cys replaced by Ala"</pre>	Key Location/Qualifiers Misc-difference 83	o nonecto.	Synthatic	Homo sabiens		arthrosteitis; fracture; achondroplasia; dvschondrogenes;	anti-arthritic activity: cartillage: octonorogic octonortheir;	pKOT279 expression vector: osteocyte: home mornhoremetic. osteocyte: beld;	Mutant MP52 monomer protein: fransforming growth factor both, man bar-	incurre manage member process.	Mittant himan Wilso manager	29-FEB-2000 (first entry)		AAY44296;	AAY44296 standard; Protein; 119 AA.	RESULT 1 AAY44296

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RESULT 2
AAW06920
ID AAW06920
XX AAW0
XX AAW0
AC AAW0
XX Unma
XX Unma
XX Huma
XX Huma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; MP52 cartilage;
                           N-PSDB;
                                                                                              Enomoto K, K
Matsumoto T,
                                                                                                                                                                                                                                17-NOV-1995;
19-APR-1995;
                                                                                                                                                                                                                                                                                                         19-APR-1996;
                                                                                                                                                                                                                                                                                                                                                               24-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                   WO9633215-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    periodontal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human MP52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW06920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW06920 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          morphogenetic, osteopathic and anti-arthritic activity. The MPS2 monomer protein is used for prevention and treatment of cartilage and/or bone diseases such as osteoporosis, osteoarthritis, arthrostetis, damage of cartilage, regeneration of bone, cartilage deficit caused by injury and tumour dissection, fracture, congenital bone and/or cartilage diseases such as achondroplasia, dyschondrogenesis, achondrogenesis, palatoschisis and dysosteogenesis and a deficit of root of teeth and a tooth socket.
                                                                                                                                                                             (FARH ) HOECHST JAPAN LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transforming them with pKOT279 expression vector containing a mutate MP52 monomer encoding nucleic acid sequence. MP52 monomer protein is capable of inducing differentiation in osteocytes and exhibits bone capable of inducing differentiation in osteocytes and exhibits bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is a mutant human MP52 monomer protein, belongs to transforming growth factor-beta (TGF-beta) superfamily. Mutant MP52 can be produced in E. coli cells by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 20; 26pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cartilage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kawai
                                                1996-485730/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000-097122/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MP52; growth factor; monomer; dimer; treatment; age; dental; disorder; fracture; bone loss; ontal disease; calcification; osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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lage diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ш
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    μ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVBSCGCR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLATROGKRPSKNIKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLATROGKRPSKNIKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   growth factor residues 383-501.
                                                                                              Katsuura
, Mikih,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kimura M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                           95JP-0322403
95JP-0093664
                                                                                                                                                                                                                                                                                                       96WO-JP01062
                                                                                                                         Z,
                                                                                            M, Kawai
Satoh Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Muraki Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for prevention
                                                                                         S, Kimura I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 649; DB 21;
Pred. No. 6.9e-60;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Katsuura M;
                                                                                            ΉX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and treatment
                                                                                                                    Makishima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein is
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RESULT 3
AAW19846
ID AAW1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                     Material for repairing bone and collagen, especially bone fracture or loss - comprising bone-inducing factor and polyoxyethylene-polyoxypropylene glycol compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is residues 383 to 501 of the human MP52 growth factor, a dimer of which can be used to treat bone, cartilage and dental disorders; including fractures, bone loss and periodontal disease. The dimer was prepared by transforming a host (preferably E. coli) with a suitable (plasmid) expression vector containing DNA encoding the monomer. The host was cultured, and inclusion bodies from the cells worked up to give the monomer, which was then converted into the dimer. The product was mixed with type 1 pig tendon collagen and injected into the large thigh vein of ICR mice. After 20 days 4 of 4 mice injected with 10 microy of the dimer showed bone/cartilage calcification around the injection site, compared to none in 0 of 4 mice treated with collagen only.
                              Example 4; Page 16-17; 31pp; Japanese.
                                                                                                                                                        Shimura T,
                                                                                                                  N-PSDB;
                                                                                                                                                                                 (FARH )
                                                                                                                                                                                                                                                 14-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                               Human; bone inducing factor; MP52; collagen; fracture;
                                                                                                                                                                                                                                                                                                                                                                                               Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW19846;
                                                                                                                                                                                                                        17-NOV-1995;
                                                                                                                                                                                                                                                                                                      WO9718829-A1
                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                      polyoxyethylene-polyoxypropylene glycol
                                                                                                                                                                                                                                                                                                                                                                                                                           12-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW19846 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide consisting of part of human MP52 growth factor, and its dimer - is used for treatment of bone, cartilage and dental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                            1997-310243/28
                                                                                                                                                                                                                                                                                                                                                                                                 bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118;
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                                                                                                                 AAT70296.
                                                                                                                                                                              HOECHST JAPAN LTD.
HOECHST PHARM & CHEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLATROGKRESKNIKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGICEFPIRSHLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLATROGKRPSKNIKARCSRKALHVNFKDMGWDDWIIAFLEYEAFHCEGLCEFPLRSHLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pages 18-19;
                                                                                                                                                                                                                                                                                                                                                                                              inducing
                                                                                                                                                     Toriyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          (first
                                                                                                                                                                                                                        95JP-0322402
                                                                                                                                                                                                                                                96WO-JP03333
                                                                                                                                                                                                                                                                                                                                                                                             factor MP52
                                                                                                                                                                                                                                                                                                                                                                                                                       entry)
                                                                                                                                                        s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 645; DB 17;
Pred. No. 1.8e-59;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Bone bone

and collagen inducing fact

inducing material

ng material has been developed which comprises polyoxyethylene-polyoxypropylene glycol

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RESULT 4
AAR78731
ID AAR7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                Oligos #6 and #7 (AAQ96218 & AAQ96219) are used as primers for the amplification of a 275 bp DNA probe, the internal 269 bp of which corresp. to nts #607 to #865 of AAQ96207, from the BMP-12 encoding plasmid subclone PCR1-1#2. This probe was radioactively labelled and used to screen a murine genomic library. DNA sequence analysis of one of positively hybridising recombinants named MVR23 indicates that it encodes a portion of the mouse gene corresp. to the PCR product mV9 (murine homolog of the MP-52 sequence AAQ96209/R78731). (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                            Oligos #6 and #7 (AAQ96218 & AAQ96219)
                                                                                                                                                                                                                                                                                                                     02-NOV-1994;
07-DEC-1993;
                                                                                                                                     Example; Page 51-52; 84pp;
                                                                                                                                                                        Bone morphogenetic proteins -12 and
                                                                                                                                                                                                           WPI; 1995-224320/29.
                                                                                                                                                                                                                                                 Celeste
                                                                                                                                                                                                                                                                       (GEMY )
                                                                                                                                                                                                                                                                                                           25-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                        06-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                      W09516035-A2
                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine protein MP52
                                                                                                                                                                                                                                                                                                                                                                               15-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-2003
23-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR78731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR78731 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        compounds. The present sequence represents human bone inducing factor MP52. This material allows treatment without surgery. It is highly absorbable because a carrier is used with the bone inducing factor, and undergoes reversible sol-gel transition depending on the
                                                                                                                                                                                                                                   Wozney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      temperature.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                  morphogenetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                   ΜŽ
                                                                                                                                                                                                                                                                                  GENETICS
                                                                                                                                                                                                                                                                       HARVARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLATROGKRPSKNIKARCSRKALHVNEKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLATROGKRPSKNIKARCSRKALHVNFKDMGWDDWIIAPLEYBAFHCEGICEFPLRSHLE
                                                                                                                                                             inducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (updated)
(first en
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                               Melton DA,
                                                                                                                                                                                                                                                                                                        94US-0333576.
93US-0164103.
94US-0217780.
                                                                                                                                                                                                                                                                                                                                                       94WO-US14030
                                                                                                                                                                                                                                                                     S INST INC.
COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                protein; MP52; tendon; ligament
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entry)
                                                                                                                                                            tendon/ligament-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.4%;
                                                                                                                                                                                                                                               Rosen
                                                                                                                                     English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 645; DB 18;
Pred. No. 1.8e-59;
0; Mismatches 1,
                                                                                                                                                                                                                                       VA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A
                                                                                                                                                                       -13
                                                                                                                                                                                                                                            Thomsen
                                                                                                                                                          and corre
                                                                                                                                                         corresp. DNA -
issue formation
                                                                                                                                                                                                                                            GH,
                                                                                                                                                                                                                                           Wolfman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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Query Match

99.48;

Score 645;

BG 16;

Length 120;

Sequence

120

Sequence

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RESULT 5
AAW26590
ID AAW2
XX AAW26590
XX AAW2
XX AW2
XX CAN
DT 25-W
DT 21-J
XX WWOUL
XW WOUL
XW WOUL
XW Ches
XX WOS
FT Prot
FT Prot
FT Prot
FT Prot
FT Prot
FT Pro
PR 25-W
XX CAN
PW 22-W
YX CAN
COLUMN COLU
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Matches 118; Conser
                                                      This polypeptide comprises human MP52. A claimed method for inducing formation of tendon and/or ligament tissues involves the administration of a composition containing at least one protein selected from MP52, BMP-12 (see AAW26599) and BMP-13 (see AAW26591). The method is used for tissue (including skin) healing and repair. This is useful for treating tendonitis, carpal tunnel syndrome and other defects of traumatic or congenital origin, in cosmetic surgery and to improve fixation of tendons or ligaments to bone. The specified proteins can also be used to increase activity of other BMPs e.g. BMP-2 (see AAW26597).
                                          BMPs e.g.
(Updated c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-DEC-1994;
07-DEC-1993;
25-MAR-1994;
02-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                  Inducing tendon and ligament formation using BMP-1 - useful for tissue healing and repair, treatment improving fixation of tendons to bone etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-424270/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wozney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Celeste
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-2003
21-JAN-1998
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HARVARD COLLEGE.
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                                                                                                                                                                                                                                                                                                                Column
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(first entry)
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93US-0164103.
94US-0217780.
94US-0333576.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e morphogenetic protein; human; tendon; ligament; cissue repair; tendonitis; carpal tunnel syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94US-0362670
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Best Local :
                        The invention relates to a chimeric DNA comprising a DNA sequence encoding a propeptide from a member of the transforming growth factor (TGF)-beta superfamily of proteins. This DNA is linked to a DNA sequence encoding an amino acid sequence encoding a mature polypeptide consisting of Bone Morphogenetic Protein (BMP)-12, BMP-13 or MP52 protein. The DNA sequences are useful for producing proteins which induce tendon/ligament like tissue formation, and for isolating and cloning further DNA like tissue formation, and for isolating and cloning further DNA sequences encoding BMP-12 related proteins with similar activity. The proteins are useful for the induction of tendon/ligament-like tissue formation, wound healing, ligament and other tissue repair, augmenting the activity of bone morphogenetic proteins, and for treating tendonitis, carpal tunnel syndrome and other tendon and ligament defects. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-DEC-1994;
07-DEC-1993;
25-MAR-1994;
                                                                                                                                                                                                                                                 New chimeric DNAs, useful for treating tendonitis, carpal tunnel syndrome and other tendon and ligament defects, comprises DNA encoding propeptide linked to DNA encoding bone morphogenetic proteins (BMP)-12, BMP-13 or MP52
                                                                                                                                                                                                                                                                                                                     WPI; 2001-588978/66.
N-PSDB; AAD18317.
                                                                                                                                                                                                                     Disclosure; Column
                                                                                                                                                                                                                                                                                                                                                                             Celeste
                                                                                                                                                                                                                                                                                                                                                                                                      (GEMY )
(HARD )
                                                                                                                                                                                                                                                                                                                                                                                                                                                02-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; MP-52; vulnerary; antiinflammatory; analgesic; ligament defect; transforming growth factor-beta; TGF-beta; tissue formation; tendonitiwound healing; tissue repair; carpal tunnel syndrome; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-1997;
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93US-0164103.
94US-0217780.
94US-0333576.
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99.2%;
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Pred. No. 1.8e-59;
0; Mismatches 1
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human MP-52 protein

The present invention relates to the isolation of human bone morphogenetic protein-12 (BMP-12) protein and a BMP-12 relate (designated BMP-13 or VL-1), and the polynucleotide sequences

protein and a BMP-12 related protein the polynucleotide sequences encoding

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RESULT 7
ABG73290
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Best Local S
Matches 118
                                                                                                    WPI; 200
N-PSDB;
                                                                                                                                                                                                                           22-DEC-1994;
28-FEB-1997;
07-DEC-1993;
25-MAR-1994;
02-NOV-1994;
                                                       New bone morphogenetic proteins (designated BMP-12) or related proteins, useful for inducing tendon/ligament-like tissue formation a patient, or for tendon/ligament-like tissue healing or repair (e.g for treating tendonitis)
                                    Claim
                                                                                                                                                                             (CELE/)
(WOZN/)
(ROSE/)
(WOLF/)
                                                                                                                                         Celeste
                                                                                                                                                                                                                                                                                                                                                                                                                        Human; bone morphogenetic protein-12; BMP-12; BMP-12 related protein BMP-13; VL-1; BMP/TGF-beta/Vg-1 family; tissue repair; tendonitis; tendon/ligament-like tissue formation; trauma induced tendon defect; tendon/ligament-like tissue healing; tendon damage; ligament damage; tendon fixation; ligament fixation; congenital; ligament defect;
                                                                                                                                                                                                                                                                                     31-AUG-2001;
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                                                     treating tendonitis)
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DB; ABX11141.
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WOZNEY J M.
ROSEN V A.
WOLFMAN N M.
THOMSEN G H.
MELTON D A.
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                                  Page 21;
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97US-0808324.
93US-0164103.
94US-0217780.
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19..120
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surgery; vulnerary; MP52.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for human MP52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.4%;
                                                                                                                                                                                                                                                                                                                                        "Specifically claimed
                                                                                                                                                                                                                                                                                                                                                          "Specifically claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .2*;
                                                                                                                                         Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 645; DB
Pred. No. 1.8e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120
                                                                                                                                       ۷A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA
                                                                                                                                       Wolfman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.8e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
                                                                                                                                       NN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                                                        in
                                                                                                                                                                                                                                                                                                                                                          in
                                                                                                                                                                                                                                                                                                                                                                                                                                                             BMP-12 related protein;
                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                        92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                          (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                     in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1119
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RESULT 8
AAR40800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                them. The novel BMPs are members of the BMP/TGF-beta/Vg-1 family of C proteins. BMP-12 and VL-1 are characterised by their ability to C induce the formation of tendon/ligament-like tissue. The BMP-12 C proteins of the invention are useful for inducing tendon/ligament-like tissue formation in a patient. They are particularly useful for tendon/ligament-like tissue healing and tissue repair, e.g. for treating tendonitis, or other tendon or ligament defects in a patient. The polynucleotide sequences encoding the BMP-12 proteins are useful for inducing tendon/ligament-like tissue formation in a patient, and for tendon/ligament-like tissue healing and tissue repair. The BMP-12 C damage to tendon or ligament tissue healing and tissue repair of tendon or ligament tissue, to improve fixation of tendon or ligament tissue, to improve fixation of tendon or ligament tissue, to repair congenital or trauma c induced tendon or ligament defects, and in cosmetic plastic surgery for attachment or repair of tendons or ligaments or ligaments. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 118
                                                                                          New transforming growth factor-beta family proteins used in tissue and wound repair, in treatment of boand tooth defects, and antibodies for diagnosis
The sequences given in AAR40800 and AAR45447 represent framents of embryo and liver derived human transforming growth factor-beta (TGF-beta) respectively. The full length protein may be used in a
                                                                                                                                                             N-PSDB;
                                                                                                                                                                        WPI; 1993-272824/34
                                                                                                                                                                                                       Hoetten G,
                                                                                                                                                                                                                                                                   12-FEB-1992;
                                                                                                                                                                                                                                                                                                                                19-AUG-1993
                                                                                                                                                                                                                                                                                                                                                             WO9316099-A2
                                                                                                                                                                                                                                                                                                                                                                                            Homo
                                                                                                                                                                                                                                                                                                                                                                                                                         organ
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGF-beta-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2003
11-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR40800
                                                                                                                                                                                                                                      (BIOP-)
                                                                                                                                                                                                                                                                                                12-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             represents human MP52.
                                                                                                                                                                                                                                                                                                                                                                                           sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                      cartilage; tooth; wound repair; immunosuppressor; transplant; cosmetic surgery; antibody; diagnosis
                                                               11; Page 19; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                      cartilage; tooth; wound repair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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                                                                                                                                                         AAQ47709
                                                                                                                                                                                                                                      BIOPHARM GES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVBSCGCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLATROGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLATROGKRPSKNLKARCSRKALHVNEKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120
                                                                                                                                                                                                        Neidhardt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone MP-52 protein.
                                                                                                                                                                                                                                                                   92EP-0102324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ÃĂ,
                                                                                                                                                                                                                                                                                                93WO-EP00350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.4%;
                                                                                                                                                                                                                                  BIOTECHNOLOGISCHEN ENTWICKL
                                                                                                                                                                                                       Ħ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 645; DB 24;
Pred. No. 1.8e-59;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ã
                                                                                                                                                                                                                                                                                                                                                                                                                                                     beta; TGF-beta; pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24;
                                                                                                            bone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                       and
                                                                                                                      DNA
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Gaps

120 119

61 60 0

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RESULT 9
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                   10-AUG-1993;
25-MAY-1994;
09-JUN-1994;
                                                                                  New DNA encoding a new member of the TGF beta family related vectors, host cells etc., has mitogenic and differentiation inducing activity, e.g. for treating or preventing diseases of bone and cartilage etc.
                                                                                                                                                                        Hotten
                                                                                                                                                                                                                                                               09-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                      Key
                                                                                                                                                                                                                                                                                                                                                                                               tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                Transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                        New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAR-2003
10-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR69600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pharmaceutical composition for the treatment of various bone, cartil or tooth defects and in tissue and wound repair processes. These proteins may also be used as immunosuppressors in organ transplants in cosmetic surgery. Antibodies raised against these proteins may bused for diagnostic purposes.

(Updated on 25-MAR-2003 to correct PN field.)
                                                               Claim
                                                                                                                                                                                                                                                                                     16-FEB-1995.
                                                                                                                                                                                                                                                                                                           WO9504819-A1
                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                           skin; mucosa;
                                                                                                                                                                                                                                                                                                                                                                                                                     treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR69600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                             (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGF-beta
                                                                                                                                                   1995-090897/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118;
                                                             6; Page 36; 51pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                         ē
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Н
                                                                                                                                                                                                                                                                                                                                                                                               regeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTNHAVIQTIMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLATROGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLATROGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE
                                                                                                                                                                         Neidhardt
                                                                                                                                                                                                                                                                                                                                                                                                                     prevention;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     401 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             growth factor-beta family; mitogenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (updated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    family member - MP-52 protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                       evention; disease; bone; cartilage; connective tissue; epithelium; dental tissue; wound healing; osteoporosis;
                                                                                                                                                                                                                   93DE-4326829.
94DE-4418222.
94DE-4420157.
                                                                                                                                                                                                                                                               94WO-EP02630
                                                                                                                                                                                                                                                                                                                             /label= mature protein
                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein;
                                                                                                                                                                     H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                                                                                                               arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.4%;
99.2%;
                                                                                                                                                                         Paulista
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 645; DB 14;
Pred. No. 7.8e-59;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                               88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ā
                                                                                                                                                                       ĭ,
                                                                                                                                                                         Hoetten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cartilage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60
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The amino acid sequence of a novel member of the transforming growth factor-beta (TGF-b) family named MP-52. The gene encodes a protein of 501 amino acids (AA). The protein, or at least the mature protein, has mitogenic and/or differentiation inducing properties useful in

or

prevention of

bone,

cartilage,

connective

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RESULT 10
AAW36100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Вb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6666<del>%</del>&
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 118
      Matches 118;
                           Query Match
                                                                 enzyme to a solution containing BMP precursor protein, or by transforming an animal cell with expression vectors containing DNA encoding the enzyme and precursor protein, culturing the transformant and isolating the mature BMP from the culture. The method can be used to produce MP52, BMP-2, BMP-4, BMP-6 and BMP-7, which can be used to treat bone formation or regeneration abnormalities.
                                                                                                                                                                                                   Production of mature bone morphogenetic protein precursor protein with a processing enzyme such directly or by expressing them both in the same
                                               Sequence
                                                                                                                                                     protein
                                                                                                                                                              The present
                                                                                                                                                                                  Example 1; Pages 21-25;
                                                                                                                                                                                                                                                          WPI; 1997-549748/50
                                                                                                                                                                                                                                                                                                      (FARH )
                                                                                                                                                                                                                                                                                                                                    30-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                  WO9741250-A1
                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                           BMP-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW36100 standard; Protein; 501 AA.
                                                                                                                                                                                                                                                                                                                                                        28-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                             06-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bone morphogenetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human MP52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      be used for wo
                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            443
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                                                                                                                                                                                                                                                                                                                                                                                                                                            BMP-4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Н
                                                                                                                                                                                                                                                                                                    HOECHST YAKUHIN KOGYO
HOECHST PHARM & CHEM F
                                                                                                                                                                                                                                                  AAT98191.
                                                                                                                                                       (AMB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         skin, mucosa, epithelium or dental tissue. The protein can all for wound healing and tissue regeneration e.g. in osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLATRQGKRPSKMLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTNEAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLATROGKRPSKNIKARCSRKALHVNFKDMGWDDWIIAPLEYEAPHCEGLCEFPLRSHLE 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR
                                              501
                                                                                                                                                                                                                                                                                 Makishima
      Conservative
                                                                                                                                                              sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       501 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first
                                             ΑĄ
                                                                                                                                                                                                                                                                                                                                                                                                                                           BMP-6;
                                                                                                                                                                                                                                                                                                                                   96JP-0130618
                                                                                                                                                                                                                                                                                                                                                        97WO-JP01474.
                                                                                                                                                                                                                                                                                                                                                                                                                                          protein; 6; BMP-7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
              99.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.4%;
                                                                                                                                                                                34pp;
                                                                                                                                                           MP52, which is a bone morphogenetic
                                                                                                                                                                                                                                                                                Takahashi M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         correct PN field.)
     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                     BMP;
   Score 645; DB 1
Pred. No. le-58;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                    Ž
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 645; DB 16
Pred. No. 1e-58;
                                                                                                                                                                                Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         processing formation;
                      DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                         enzyme; MP52;
bone regenera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                     - by treatment as furin either host
                      Length 501;
                                                                                                                                                                                                                                                                                                                                                                                                                                        regeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The protein can also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              501;
  0
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 Gaps
                                                                                                                                                                                                                         Of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119
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0;
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PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR

PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVXKQYEDMVVESCGCR

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AAW19210
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                                                              Query Match
Best Local Similarity
Matches 118; Conserv
                                                                                                                                      This sequence is the human transforming growth factor (TGF)-beta protein designated MP52. MP52 can be used in a compound of formula (I):

A-X(I-20)-B(I-20) (I); A = protein, or fragment, of the TGF-beta superfamily with cartilage and/or bone inducing activity (e.g. MP52);

B = 1 or more substituent groups with an affinity to the extracellular matrix, cellular components of bone and/or cartilage and/or to a biocompatible carrier matrix; X = 1 or more covalent bonds and/or spacer groups. The compound may be used to inhibit bone resorption, prevent or treat bone or cartilage related disorders, including osteoporosis, Paget's disease, osteodystrophy, osteoarthritis or osteoarthropathy and to treat bone or cartilage damage caused by wounding or overloading.
                                                                                                                                                                                                                                                                                                                                                  Compound containing protein from TGF-beta superfamily - has bone and/or cartilage inducing activity, useful in treatment of, e.g. osteoporosis, bone damage, Paget's disease and osteoarthritis
                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bechtold R,
                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-333931/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human transforming growth factor-beta; TGF-beta; MP52; superfamily; cartilage; bone inducing activity; inhibit; bone resorption.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BIOP-) BIOPHARM GES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-DEC-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-JUN-1997.
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      383
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                                                                                                                                                                                                                                                                                                                           3; Page 9; 10pp;
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PLATROGKR PSKNLKARCSEKALHVNEKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE
                        PLATROGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLATROGKRPSKNIKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLATROGKRESKNLKARCSRKALHVNEKDMGWDDWIIAPLEYEAFHCEGLCEEPLRSHLE
                                                                                                                      501 AA;
                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hotten
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                                                                         99.4%;
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                                                                                                                                                                                                                                                                                                                              German.
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                                                             0
                                                        Score 645; DB 1:
Pred. No. 1e-58;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pohl J,
                                                                                       DB 18;
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                                                                                     Length
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RESULT 12
AAW11900
ID AAW11
XX AAW11
XX AAW11
XX AAW11
XX AAW11
XX AAW11
XX Growt
KW Growt
KW Growt
KW Wound
XX Homo
XX WO970
YX WO970
YX YOF 24-JU
YX (FARE
PA (FARE)
PT (FARE)
PT (FARE
PT (FARE)
PT (FAR
          RESULT 13
AAW01799
ID AAW01
XX
AC AAW01
XC AAW01
XX
DT 15-OC
XX
DE Human
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KW Human
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Best Local,
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                                      Human MP52 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW11900 is a high mol. wt. form of a human growth/differentiation factor MP52 MP52 promotes bone induction and is useful for plastic reconstructive surgery, cosmetic facial treatment, bone transplantation and tooth implantation. It is also useful for the treatment and prevention of disorders of bone formation, bone, cartilage, joint tissue, skin, mucous membranes, nails or teeth; for wound treatment and tissue regeneration; and for the treatment of skeletal disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 199
N-PSDB;
      Human; MP52; transforming
                                                                                                                                       AAW01799
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                          15-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 12-16; 25pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High molecular weight hur promotes bone induction,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fujino
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                                                                                                                                                                                                                                                                                                                                  Mu
Local 118;
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DB; AAT61412.
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                                                                                                                                                                                                                                                                                                                                                                Similarity
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HOECHST PHARM & CHEM
                                                                                                                                                                                                                                       PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVXKQYEDMVVESCGCR
                                                                                                                                                                                                                                                                            PLATROGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLBYEAFHCEGLCEFPLRSHLB 442
                                                                                                                                     standard;
                                                                                                                                                                                                              PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR
                                                                                                                                                                                                                                                                                                PLATROGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYBAFHCEGLCEFFLRSHLE
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                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                        (first
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joint tissue; cartilage; mucous m
regeneration; skeletal disorder;
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                                                                                                                                   Protein;
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on, is
      growth
                                                                                                                                     501
                                                                                                                                                                                                                                                                                                                                          Score 645; DB 18
Pred. No. 1e-58;
0; Mismatches
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      factor;
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      TGF;
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     beta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                osteoporosis; teeth;
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     medicament;
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Mat_protein
                                                                                                                                                                                   Bone morphogenic factor; MP52 Arg; bone; cartilage; skin; connective tissue; mucous membrane; epithelium; teeth; wound healing; vulnerary; tissue regeneration; osteoporosis; bone fracture; dental implant; osteoblast.
                              Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is the human MP52 protein, which is described in WO 9316099 and 9504819 as a member of the human transforming growth factor beta superfamily. Active MP52 can be used in a medicament to treat and prevent nervous system diseases, and/or to treat neuropathological conditions caused by nervous system ageing.
                                                                             Cleavage-site
                                                                                                                                                                                                                                                                       Human bone morphogenic factor MP52 Arg.
                                                                                                                                                                                                                                                                                                         11-MAY-1997
                                                                                                                                                                                                                                                                                                                                       AAW12770;
                                                                                                                                                                                                                                                                                                                                                                      AAW12770 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                             Peptide
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                                                                                                                                                           sapiens
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/note= "; 381..501
        /note= "sequencing suggests MP52 Arg is processed 381..382 "alternative cleavage site at Arg381-Ala382 'note= "alternative cleavage site at Arg381-Ala382
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                                                                           380..381
                                                                                                               Location/Qualifiers
1..27
                                                                                         /label= Sig_peptide
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Pred. No. 1e-58;
0; Mismatches
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ID AAW44
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Matches 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       maturation of osteoblasts. It is effective for treating/preventing bone diseases caused by abnormal bone metabolism such as osteoporosis. It also accelerates the healing of bone fractures, and is useful for orthopaedic reconstruction, bone transplantation, and dental therapeutics because of its bone morphogenetic activity. It is also effective for preventing/treating cartilage, skin, connective tissue, mucous membrane, teeth and epithelial disorders. Recombinant Mp52 Arg can be produced in host (e.g. CHO) cells utilising an isolated DNA sequence (AAT59729) in plasmid pMSS99.
                           19-NOV-1996;
                                                                                20-MAY-1998
                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                              TGF-beta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW44868 standard; protein; 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human bone morphogenic factor MP52 Arg (AAW12770) is a growth factor that induces formation of cartilage from undifferentiated mesenchymal cells and which stimulates the differentiation and maturation of osteoblasts. It is effective for treating/preventing
                                                                                                                                 DE19647853-A1
                                                                                                                                                                                                                                                                                                                                                                         24-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                              AAW44868;
                                                                                                                                                                                                                                     bone replacement;
                                                                                                                                                                                                                                                                                                               TGF-beta superfamily subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-AUG-1995;
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ches 118;
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                                                                                                                                                                                                                                                              calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 501 AA;
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                           96DE-1047853
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/note= "mature MP52
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cartilage; bone; ;
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                                                                                                                                                                                                                                     fracture
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                                                                                                                                                                                                                                                                                                                                                                                                                             Bioactive implant material for bone osteogenic calcium phosphate matrix
                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Page 8-10; 12pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-287890/26
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(GERO-)
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                                                                                                                 PLATROGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE
                                                                                                                                        PLATROGKRPSKNIKARCSRKALHVNFKDMGWDDWIIAPLEYBAFHCEGLCEFPLRSHLE
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Result
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US-08-945-459A-1

Sequence 1, Application US/08945459A Publication No. US20020102633A1

GENERAL INFORMATION:

APPLICANT: MAKISHIMA, FUSAO; TAKAMATSU,
APPLICANT: HIROYUKI, MIKI, HIDEO; KAWAI,
APPLICANT: SHINUI; KIMUSA, MICHOI; MATSUMOTO,
APPLICANT: TOMOAKI; KATSUURA, MIEKC; ENOMOTO,
APPLICANT: KOICHI; SATOH, YUSUKE
TITLE OF INVENTION: A NOVEL PROTEIN AND
TITLE OF INVENTION: PROCESS FOR PREPARING THE
NUMBER OF SEQUENCES: 4

SAME

CORRESPONDENCE ADDRESS:

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equence	37,	equence 15,	e 37,	e 10	e 15	e 13,	e 13	equence 15,	equence 30	e 61	equence 12,	equence 28	equence 34	equence 2,	e 75	equence 73	e 76	equence 72	e 57	e 14	ce 14	14,	`	32,	e 6,	e 20,	equence 26,	equence 74,	

### ALIGNMENTS

ADDRESSEE: BIERMAN, MUSERLIAN AND LUCAS
ADDRESSEE: LLP
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: MICROSOFT WORD 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/945,459A
FILLING DATE: 19-AER-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/01062
FILLING DATA: 19-AER-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP7/322403
FILLING DATE: 17-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP7/322403
FILLING DATE: 17-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP7/33664
FILLING DATE: 119-AER-1996

TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 661-8000

(212) 661-8002

REGISTRATION NUMBER: 19, REFERENCE/DOCKET NUMBER:

19,683

146.1275

ATTORNEY/AGENT INFORMATION:

CHARLES A. MUSERLIAN

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US-09-068-253-2
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                                                                                                                                                                                                                                                           SEQ ID NO 2
LENGTH: 119
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APPLICANT: SHIMURA, Takesada
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09068253
Patent No. US20020168381A1
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                                                                                                                                          Matches
                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                         APPLICANT: TORIYAMA, Satsuki
TITLE OF INVENTION: CARTILAGE/ BONE INDUCING MATERIALS FOR REPARATION
FILE REFERENCE: 146.1286
CURRENT APPLICATION NUMBER: US/09/068,253
CURRENT FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: PCT/JP96/03333
PRIOR FILING DATE: 1996-11-14
PRIOR FILING DATE: 1995-11-17
NUMBER: JP 7/322402
PRIOR FILING DATE: 1995-11-17
NUMBER: OF SEQ. ID NOS: 4
                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 119 AMINO ACIDS
                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
ORIGINAL SOURCE:
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LOCATION:
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                                                                                                                                        118;
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                                                                                             1 PLATROGKRPSKNIKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGICEFPIRSHIE 60
                                                                                                                                                         Similarity
                       PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
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                                                                   PLATROGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
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PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
                                                                                                                                        Conservative
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383 TO 501
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Pred. No. 1.8e-62;
0; Mismatches 1;
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                                                                                                                                                                     Length 119;
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                                                                                                                                                                     Matches
                                                                                                                                                                                       Query Match
Best Local (
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION NUMBER: PCT/JP96/01062

FILING DATE: 19-APR-1996

APPLICATION NUMBER: JP7/322403

FILING DATE: 17-NOV-1995

APPLICATION NUMBER: JP7/93664

FILING DATE: 19-APR-1995

APPLICATION NUMBER: JP7/93664

FILING DATE: 19-APR-1995

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/365,231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: MAKISHIMA, FUSAO; TAKAMATSU,
HIROYUKI; MIKI, HIDBO; KAWAI,
SHINUI; KIMURA, MICHIO; MATSUMOTO,
TOMOAKI; KATSUURA, MIEKO; ENOMOTO,
KOICHI; SATOH, YUSUKE
                                                                                                                                                                                                                                                                     NAME/KEY: MP52
LOCATION: 383 TO 501
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
ORGANISM: HOMOSAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: LINEAR MOLECULE TYPE: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: A NOVEL PROTEIN AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                   118;
61
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                                                                                                                                                                                       Similarity
                                                                                                                    PLATROGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYBAFHCBGLCEFPLRSHLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: MICROSOFT WORD 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: NEW YORK
STATE: NEW YORK
                        PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
                                                                                  PLATROGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
                                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 119 AMINO ACIDS
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212) 661-8000
TELEPAX: (212) 661-8002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 600 THIRD AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: BIERMAN, MUSERLIAN AND LUCAS
PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: CHARLES A. MUSERLIAN
                                                                                                                                                                                                                                                                                                                                                            TISSUE TYPE:
                                                                                                                                                                   Conservative
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                                                                                                                                                                 Score 645; DB 12;
Pred. No. 1.8e-62;
0; Mismatches 1;
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                                                                                                                                                                                                           Length 119;
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                                                                                                                                                                         Sequence 4, Application US/09945182 Patent No. US20020160494A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Publication No. US20040019185A1
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PRIOR FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 09/701,121
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: PCT/BP00/07600
PRIOR PILING DATE: 2000-08-04
PRIOR PILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: 09/331,948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: PROCESS FOR PREPARING PURIFIED ACTIVE MONOMER OF TITLE OF INVENTION: BONE-DERIVED FACTOR FILE REFERENCE: 146:1320-1
CURRENT APPLICATION NUMBER: US/10/414,954
CURRENT FILING DATE: 2003-04-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ANDOU, HIDETOSHI
APPLICANT: HONDA, JUN
APPLICANT: SUGIMOTO, SJUNJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 1996-12-25
NUMBER OF SEQ ID NOS: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: PCT/JP97/04784 PRIOR FILING DATE: 1997-12-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: JP 10 141379
PRIOR FILING DATE: 1998-05-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: JP 8 355812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: if dimeric human MP52 variant, Xaa is cysteine; if OTHER INFORMATION: monomeric human MP52 variant, Xaa is any amino acid OTHER INFORMATION: except cysteine and preferably alanine, serine, OTHER INFORMATION: threonine, leucine, isoleucine, glycine or valine
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                Thomsen, Gerald H.

Melton, Douglas A.

TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER
                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
SEQUENCES: 35
                                                                     Wozney, John
Rosen, Vicki A.
Wolfman, Neil
                                                                                                                               Celeste, Anthony J. Wozney, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JENS
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99.2%;
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Pred. No. 1.8e-62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 119;
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APPLICANT: Pohl, Jens
APPLICANT: Bechtold, Rolf
APPLICANT: Bechtold, Michael
APPLICANT: Paulista, Michael
APPLICANT: Unsicker, Klaus
TITLE OF INVENTION: USE OF MP52 OR MP121 FOR TR
TITLE OF INVENTION: USEVOUS SYSTEM
FILE REFERENCE: 100564-07032
CURRENT APPLICATION NUMBER: US/08/981,490B
CURRENT APPLICATION NUMBER: PCT/EP96/03065
PRIOR APPLICATION NUMBER: PCT/EP96/03065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/089814908 Publication No. US20020045568A1
                                                                SOFTWARE: PatentIn version SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                               NUMBER OF SEQ ID NOS:
                                                                                                                                  PRIOR APPLICATION NUMBER: DE/195 25 416.3 PRIOR FILING DATE: 1995-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                       LENGTH: 501
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Sim hes 118;
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ADDRESSES: GENETICS INSTITUTE,
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/808,324
FILING DATE: <Unknown>
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/945,182
FILING DATE: 31-Aug-2001
CITCHILDER: D1-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 120 amino acids
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Pred. No. 1.8e-62;
0; Mismatches 1;
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-164-279-53
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US-10-164-279-53
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Best Local Similarity
Matches 118; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Keck, P.
TITLE OF INVENTION: MORPHOGEN ANALOGS OF I
FILE REFERENCE: CIBT-P04-566
CURRENT APPLICATION NUMBER: US/10/164,279
CURRENT FILING DATE: 2002-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/10356513
Publication No. US20030220248A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 53, Application US/10164279 Publication No. US20030185792A1
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  SOFTWARE: PatentIn
SEQ ID NO 1
                                                                                                                                                                                                                                       APPLICANT: Hotten, Gertrud
APPLICANT: Pohl, Jens
APPLICANT: Pohl, Jens
APPLICANT: Bechtold, Rolf
APPLICANT: Baulista, Michael
APPLICANT: Unsicker, Klaus
TITLE OF INVENTION: The Use Of MP52 Or MP121
TITLE OF INVENTION: The Nervous System
FILE REFERENCE: 2923-0127
TITLE DESIGNATION: THE NERVOUS SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 09/791946
PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 64
                                                                                                           CURRENT APPLICATION NUMBER: US/10/356,513
CURRENT FILING DATE: 2003-02-03
PRIOR APPLICATION NUMBER: US 08/981490
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: PCT/EP96/03065
PRIOR FILING DATE: 1996-07-12
PRIOR FILING DATE: 1996-07-12
                                            PRIOR APPLICATION NUMBER: DE 195 25 416
PRIOR FILING DATE: 1995-07-12
NUMBER OF SEQ ID NOS: 5
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Pred. No. 9.2e-62;
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Pred. No. 9.2e-62;
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APPLICANT: Bechtold, Rolf
APPLICANT: Bechtold, Rolf
APPLICANT: Bechtold, Rolf
APPLICANT: Bechtold, Rolf
APPLICANT: Paulista, Michael
APPLICANT: Unsicker, Klaus
TITLE OF INVENTION: The Use Of MP52 Or MP121 For Treating And
TITLE OF INVENTION: The Nervous System
FILE REFERENCE: 2923-0127
CURRENT APPLICATION NUMBER: US/10/356,513
CURRENT ELLING DATE: 2003-02-03
PRIOR APPLICATION NUMBER: US 08/981490
PRIOR APPLICATION NUMBER: PCT/EP96/03065
PRIOR APPLICATION NUMBER: DCT/EP96/03065
PRIOR APPLICATION NUMBER: DCT/EP96/03065
PRIOR APPLICATION NUMBER: DCT/EP96/03065
PRIOR FILING DATE: 1996-07-12
PRIOR FILING DATE: 1995-07-12
PRIOR FILING DATE: 1995-07-12
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US-09-880-708-13
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                                                                                                                                                                            Sequence 13, Application US/09880708 Patent No. US20020165361A1 GENERAL INFORMATION:
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Best Local Similarity
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Publication No. US20030220248A1
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Best Local Similarity
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TYPE: PRT
ORGANISM: Human
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                                                            TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                       APPLICANT:
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                       ADDRESSEE: Gray Cary Ware
STREET: 4365 Executive Dri
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San Diego
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                                                                                                                                  Huynh,
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Pred. No. 9.2e-62;
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Pred. No. 9.2e-62;
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RESULT 11
US-09-880-708-10
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Patent No. US20020165361A1
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
Huynh, Thanh
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les 117; Conserv
                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Gray Cary Ware & Freidenrich LLP
STREET: 4365 Executive Drive, Suite 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 09/145,060
FILING DATE: <UNKNOWN:
APPLICATION NUMBER: 08/03,144
FILING DATE: 12-JAN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                          ZIP: 92121-2189
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/880,708
FILING DATE: 12-Jun-2001
                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/880,708
FILING DATE: 12-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                    HUYDH, THARH
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 07265/057002
TELECOMMUNICATION INFORMATION:
                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/145,060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE DESCRIPTION: SEQ ID NO: 13:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLATROGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 858/677-1456
TELEFAX: 619/677-1465
NN FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Lisa A. Haile, Ph.D. REGISTRATION NUMBER: 38,347
                                                                                                                COMPUTER: IBM Compatible OPERATING SYSTEM: Windows95 SOFTWARE: FastSEQ for Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLANROGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE
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OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                 CITY: San Diego
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 119 amino acids TYPE: amino acid
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DATE: <Unknown>
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98.3%;
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Pred. No. 6.3e-62;
0; Mismatches 2;
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                                                                                                                                                              Matches
                                                                                                                                                                                 Query Match
Best Local |
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CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: PCT/US99/05908
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: PCT/US98/19772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Bruce D. Weintraub
APPLICANT: Mariusz W. Szkudli
APPLICANT: University of Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Mariusz W. Szkudlinski
APPLICANT: University of Maryland
TITLE OF INVESTION: CYSTILE KNOT GROWTH FACTOR MUTANTS
FILE REFERENCE: UOFMD.003C1
                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 1998-09-22
NUMBER OF SEQ ID NOS: 41
                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: HOMO SAPIEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                     LENGTH: 502
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REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/057002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858/677-1456
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FILING DATE: 12-JAN-1993
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE DESCRIPTION:
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                                                                             384 PSATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE
                                                                                                                                                           117;
444 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR
                                     61
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                                                                                                                                                                              Similarity
                           PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLANROGKRPSKNLKARCSRKALHVNFKDMGWDDWITAPLEYEAFHCEGLCEFPLRSHLE 436
                                                                                                       PLATROGKRESKNIKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 495 amino acids
TYPE: amino acid
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98.3%;
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Pred. No. 3.2e-61;
0; Mismatches 2;
                                                                                                                                                                            Score 639; DB 10;
Pred. No. 4.1e-61;
                                                                                                                                                           Mismatches
                                                                                                                                                                                               DB 10;
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  502
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RESULT 13 US-09-730-772-13 ; Sequence 13, Ap

; Sequence 13, Application US/09730772 ; Patent No. US20010011131A1

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RESULT 14
US-09-735-849-13
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                                                                                                                                                                                                                                       Sequence 13, Application US/09735849 Patent No. US20010037017A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 116;
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Best Local Similarity
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APPLICANT: Luyten,
APPLICANT: Moos, J.
APPLICANT: Chang,
                                                                                                                          GENERAL INFORMATION:
APPLICANT: Luyten, Frank P.
APPLICANT: Moos, Jr., Malcolm
APPLICANT: Chang, Steven Chao-Huan
TITLE OF INVENTION: CARTILAGE-DERIVED MORPHOGENETIC
TITLE OF INVENTION: PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 501 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: NI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION: NAME: Bartfeld, Neil S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/730,772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: CARTILAGE TITLE OF INVENTION: PROTEINS NUMBER OF SEQUENCES: 24 CORRESPONDENCE ADDRESS:
                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER:
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 39,901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE
 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                      443
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                   Newport Beach
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620 Newport Center Drive, 16th Floor
                                                    E: Knobbe, Martens, Olson & Bear
620 Newport Center Drive, 16th Floor
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Chang, Steven Chao-Huan
Chang, Steven Chao-Huan
VENTION: CARTILAGE-DERIVED MORPHOGENETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U.S.A.
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U.S.A.
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Pred. No. 5.1e-60;
"" amatches 3;
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RESULT 15
US-10-379-830-13
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; MOLECULE TYPE:
US-09-735-849-13
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Bartfeld, Neil S
REGISTRATION NUMBER: 39,901
REFERENCE/DOCKET NUMBER: NIH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOSTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/735,849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Luyten, Frank P.
Moos, Jr., Malcolm
Chang, Steven Chao-Huan
TITLE OF INVENTION: CARTILAGE-DERIVED MORPHOGENETIC
            COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/379,830
FILING DATE: 03-Max-2003
CLASSIFICATION: -UNKnown-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/730,772
                                                                                                                                                                                              ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 24 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          383 PSATROGKRPSKNÍKÁRČSRKÁLHVNFKDMGWDDWITAPLEYBAFGCBGLCBFPLRSHLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           443 PTNHAVIQTLMNSMDÞESTÞÞTCCVÞTRLSÞÍSÍLFIDSANNVVYKQYEDMVVESCGCR 501
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                                                                                                                                                                                                                                                                             STATE: CA
                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, 16th Floor
FILING DATE: 30-NOV-2000
                                                                                                                                                                                                                                                        COUNTRY: U.S.A.
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linear
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97.5%;
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Pred. No. 5.le-60;
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APPLICATION NUMBER: 08/836,081

ATTORNEY/AGENT INFORMATION:

NAME: Bartfeld, Neil S

REGISTRATION NUMBER: 39,901

REFERENCE/OCCKET NUMBER: NIH099.001APC

TELEPHONE: 619-235-0550

TELEPHONE: 619-235-0550

TELEPHONE: 619-235-0550

TELEPHONE: 619-235-0176

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
SEQUENCE DESCRIPTI
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Scoring table: Sequence: Title: Perfect score:

protein on:

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Maximum Minimum Total number

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Database

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1: /cgm2 6/ptodata/1.
2: /cgm2 6/ptodata/1.
3: /cgm2 6/ptodata/1.
4: /cgm2 6/ptodata/1.
5: /cgm2 6/ptodata/1.
6: /cgm2 6/ptodata/1.
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 Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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/cgm2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgm2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgm2_6/ptodata/1/iaa/FCTUS_COMB.pep:*
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US-08-333-576C-4
US-08-38-324-4
PCT-US94-14030A-4
PCT-US94-526B-3
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US-08-981-490B-1
US-08-981-490B-1
US-08-455-59-13
US-09-145-060-13
PCT-US94-00657-13
US-09-145-060-13
US-09-145-060-13
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US-08-288-508C-51
US-08-288-508C-7
US-08-288-508C-7
US-08-288-508C-7
US-08-288-508C-7
US-08-581-529B-7
US-09-097-616-7
PCT-US94-07762-6
US-09-097-616-6
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US-08-362-670B-4
; Sequence 4, App
; Patent No. 5658
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                                              Query Match
Best Local Similarity 99.7
Matches 118; Conservative
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                                                                                                                                                                                                       TELEPHONE: 617 498-8260
TELEFAX: 617 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 520
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
TELEPHONE: 617 498-8260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Celeste, Anthony J.
APPLICANT: Wozney, John
APPLICANT: Rosen, Vicki A.
APPLICANT: Thomsen, Neil
APPLICANT: Thomsen, Gerald H.
APPLICANT: Melton, Douglas A.
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: December:
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 87
CITY: Cambr
STATE: Mass
COUNTRY: US
ZIP: 02140
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                                                                                                                                                          TOPOLOGY:
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amino acid
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US-08-362-670B-32
US-08-333-576C-32
PCT-US94-14030A-32
US-08-360-914B-15
US-08-360-914B-15
US-08-360-670B-2
US-08-362-670B-2
US-08-362-670B-2
US-08-362-670B-34
US-08-362-670B-34
US-08-362-670B-34
US-08-333-576C-2
US-08-333-576C-3
US-08-333-576C-3
US-08-333-576C-3
US-08-333-576C-3
US-08-333-576C-38
US-08-333-576C-28
US-08-333-576C-28
US-08-333-576C-28
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                                                      Score 645; DB
Pred. No. 1.4e
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Score

DB 1; ..4e-64;

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; Sequence 4, Application
; Patent No. 6284872;
; GENERAL INFORMATION:
APPLICANT: Celeste,
APPLICANT: Wozney,
APPLICANT: Rosen,
                                                                                                                       US-08-808-324-4
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US-08-333-576C-4
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                                                                                                                                         RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-333-576C-4
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                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 118; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 617 876-5851
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 617 498-8260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: No. 6027919ember 2, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MG-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: TE NUMBER OF SEQUENCES: 3 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Melton, Douglas A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/333,576C
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87 CambridgePark Drive
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Rosen, Vicki A.
Wozney, John
Rosen, Vicki A.
Wolfman, Neil
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                                                   Anthony J
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                                                                                                                                                                                                                                                                                                                             Score 645; DB 3;
Pred. No. 1.4e-64;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                  Length 120;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,324
FILING DATE: Herewith
CLASSIFICATION: 114
ATTORNEY/AGENT INFORMATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5202-D
TELEPHONE: 617 498-8260
TELEPHONE: 617 498-8260
TELEPHONE: 617 876-5851
INFORMATION FOR SEQ ID NO: 4:
CECHTRICE CHARACTERISTICS:
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                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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LENGTH: 120 amino acids
TYPE: amino acid
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: GENETICS INSTITUTE,
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                       APPLICANT: GENETICS INSTITUTE, INC.
APPLICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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PRIOR APPLICATION DATA
                                                                                                                                                                                                                         STREET: 6, Cambridge
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                   CLASSIFICATION:
                                   APPLICATION NUMBER: FILING DATE: Herew
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                                                                                                                                                                                                         COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
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                                     Herewith
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Pred. No. 1.4e-64;
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US-08-289-222E-3
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                                                                                                                                                                                        ZIP: 20005-5701

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/289,222E

FILING DATE: 25-AUG-1999
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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NAME: Lazar, Steven R.
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM
STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
STREET: SUITE 330
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                                               APPLICATION NUMBER: DE P
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
                                                                                                  APPLICATION NUMBER: US 0 FILING DATE: 12-AUG-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS OF THE TGF-B TITLE OF INVENTION: FAMILY
                                                                                                                                                       CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                        STREET:
CITY: W
STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/164,103
FILING DATE: 07-DEC-193
APPLICATION NUMBER: US 08/217,780
FILING DATE: 25-MAR-1994
                 APPLICATION NUMBER: EPO
FILING DATE: 12-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/333,576 FILING DATE: 02-NOV-1994
                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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APPLICATION DATA:
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20005-5701
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BECHTOLD, ROLF
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                                EPO 92102324.8
                                                                                                                                          US 08/289,222
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No. 1.4e-64;
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0; Mismatches
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RESULT 6
US-09-054-526B-3
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APPLICANT: H TTEN
APPLICANT: NEIDHA
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                                                                                                                  APPLICATION NUMBER: US 08/
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P
FILING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: BECHTOLD,
APPLICANT: POHL, JEN
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 36,105
REPERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MONICA CHIN
                                                                                                                                                                                                                           FILING DATE: 03-APR-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/054,526B
                                                                                                                                                                                                                                                                                                                                                ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: NIKAIDO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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STREET:
CITY: W
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Local Similarity 99.2%;
nes 118; Conservative
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                                                                                    APPLICATION NUMBER: FILING DATE: 12-FEB
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                                                                                                                                                                                                                                                                                                                                                                                                                          DC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            401 amino acids
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BECHTOLD, ROLF
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                                                                                                       EPO 92102324.8
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Pred. No. 6.2e-64;
0; Mismatches 1
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/288,500 FILING DATE: 10-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
                             REFERENCE/DOCKET NUMBER: P564-4019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-5000
TELEPAX: (202)638-4810
                                                                                                                                                                                                                  APPLICATION NUMBER: DE P
FILING DATE: 10-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P
FILING DATE: 25-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: H tten, Gertrud
APPLICANT: Neidhardt, Helge
APPLICANT: Paulista, Michael
APPLICANT: Paulista, Michael
                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATING FACTOR TITLE OF INVENTION: THE TGF- FAMILY NUMBER OF SEQUENCES: 40
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                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                     NAME: JAHNS, Kristina M.
REGISTRATION NUMBER: P-41,092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A. ZIP: 20005-5701
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                                                                                                                                                                 FILING DATE: 09-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D.C.
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Pred. No. 6.2e-64;
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LENGTH: 501
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity 99.2
Matches 118; Conservative
                                                                                                                                                                              Sequence 13, Applicat Patent No. 5801014
GENERAL INFORMATION:
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APPLICANT: Pohl, Jens
APPLICANT: Bechtold, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/08/981,490B
CURRENT FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: PCT/EP96/03065
PRIOR FILING DATE: 1996-07-12
PRIOR APPLICATION NUMBER: DE/195 25 416.3
PRIOR FILING DATE: 1995-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: USE OF MP52 OR MP121 FOR TREATING AND PREVENTING DISEASES OF THE TITLE OF INVENTION: NERVOUS SYSTEM FILE REFERENCE: 100564-07032
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn version 3.1
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                                                                                                    APPLICANT: LEE, SE-JIN
APPLICANT: HUYNH, THANK
TITLE OF INVENTION: GRO
NUMBER OF SEQUENCES: 2'
                                                                                     CORRESPONDENCE ADDRESS:
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TOPOLOGY:
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                               ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              443 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       383 PLATROGKRÞSKNLKARĆSRKÁLHVNFKDMGWDDWITAPLEYEAFHCEGLCEFPLRSHLE 442
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                                                                                                                                                                                                 13, Application US/08455559
5. 5801014
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Similarity 99.2%;
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Unsicker, Klaus
                   CALIFORNIA
SD
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                                                                                                        GROWTH DIFFERENTIATION FACTOR-5
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Pred. No. 8.3e-64;
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Pred. No. 8.3e-64;
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Best Local S
Matches 117
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 13, Application US/09145060 Patent No. 6245896
                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: Huynh, Thanh
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 13:
                                                                    OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
NAME: WETHERELL, JR. PH.D., JOHN R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD2280
                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/003,144
                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: prot
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                      STREET:
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MEDIUM TYPE: Floppy disk
                                                     APPLICATION NUMBER:
                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
 APPLICATION NUMBER:
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                                                                                                                                                                                                                                                      4225 Executive Square,
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08/455,559
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                                                 US/09/145,060
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                                                                                                                                                                                                                                                      Suite 1400
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PCT-US94-00657-13
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Matches 117; Conservative
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TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO:
STKAND.
TOPOLOGY: line...
MOLECULE TYPE: pro
IMMEDIATE SOURCE:
TYPNE: GDF-5
                                                                                                                                                        TELEPHONE: 619/455-510
TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                        NAME: WETHERELL, JR. PH.D.,
REGISTRATION NUMBER: 31,678
REFERENCE, DOCKET NUMBER: PD3
TELECOMMUNICATION, INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
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CLONE: GDF-5
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: WETHERELL, JR. PH.I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
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                                                           STRANDEDNESS: SIL
                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: I
FILING DATE: 1/12/94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 31-MAY APPLICATION NUMBER:
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ZIP: 90067
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                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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                                                                                                                    119 amino acids
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98.3%;
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Pred. No. 4.9e-64;
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US-08-455-559-10
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US-08-455-559-10
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Best Local Similarity
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NAME: WETHERELL, JR. PH.D., J
REGISTRATION NUMBER: 31.678
REFERENCE/DOCKET NUMBER: 2D22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/455-5100
                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/003,144
FILING DATE: 12-JAN-1993
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APPLICANT: HUYNH, THANH
TITLE OF INVENTION: GROWTH DIFFERENTIATION FAC
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
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LOCATION:
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FILING DATE: 31-MAY-1995
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les 117; Conservative
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                                                                      PLANROGKRPSKNIKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 436
PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR
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                                                                                                                                                                                                                                                                                        495 amino acids
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                                                                                                                                               Conservative
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                         linear
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: GROWTH DIFFERENTIATION FACTOR-5
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                                                                                                                                         Score 640; DB 1; Length 495; Pred. No. 2.9e-63; O; Mismatches 2; Indels
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US-09-145-060-10
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PCT-US94-00657-10
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                                                                                                                                                                                         Sequence 10, Application PC/TUS9400657 GENERAL INFORMATION:
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Best Local :
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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FILING DATE: 31-MAY-1995
APPLICATION NUMBER: 08/00:
FILING DATE: 12-UAN-1993
ATTORNEY/AGENT INFORMATION:
NUMBER: 11:50 MIGGINETION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Lisa A. Haile, Ph.D. REGISTRATION NUMBER: 38,347 REFERENCE/DOCKET NUMBER: 07. TELECOMMUNICATION INFORMATION: TELEPHONE: 619/678-5070
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SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Executive Square, Suite 1400
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                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
                                                                                                                                  APPLICANT: SE-JIN LEE
APPLICANT: HUYNH, THANH
TITLE OF INVENTION: GROV
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                                                                                                                NUMBER OF SEQUENCES:
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                                    CITY: LOS ANGELES
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al Similarity 98.3%;
117; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                              1 PLATROGKRPSKNIKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE
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1: CA
FRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92037
                                                                                                                                                                                                                                                                                                                                              PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
                                                                                                                                                                                                                                                                                                                                                                                         PLANROGKRPSKNIKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE
CALIFORNIA: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GROWTH DIFFERENTIATION FACTOR-5
27
                                                                                                                                  GROWTH DIFFERENTIATION FACTOR-5
                                                                                                                    27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08/003,144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08/455,559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 640; DB 3;
Pred. No. 2.9e-63;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07265/057001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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RESULT 15
US-08-335-583C-51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 51, Application US/08335583C Patent No. 5693779 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 117; Conserv
                                                                                                                                                                                                                                              STALL
COUNTRY: USA
CIP: 92660
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: TYSTEM: DOS
                                                                                                                   SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/335,5:
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIPTOTAL

LEGISLA COLORS TO THE COLORS SOFTWARE: PATENTING PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Verification DATA:

APPLICATION NUMBER: PCT/US94/00-TEILING DATE: 1/10/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
ATTORNEY AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: NII
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Moos Jr., Malcolm
APPLICANT: Wang, Shouwan
APPLICANT: Wang, Shouwan
APPLICANT: Krinks, Marie
TITLE OF INVENTION: PRODUCTION AND USE OF
TITLE OF INVENTION: ANTI-DORSALIZING MORPHOGENETIC PROTEIN
NUMBER OF SEQUENCES: 56
                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: WETHERELL, JR. PH.D.,
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: FD3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                              CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       437 PÍNHAVÍQTÍMNSMDÞESTÞÞTCCVÞTRÍSÞÍSIÍFÍDSANNVVYKQVEDMVVESCGCR 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 PTNHAVIQTEMNSMDEESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLANRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        495 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98.6%;
                                                                                                                                                                                               US/08/335,583C
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                        NIH104.001A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 640; DB 5; Length 495; Pred. No. 2.9e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOHN R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Version
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Search completed: February 18, 2004, 17:44:26 Job time : 21 secs
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                                                                                                                                                                                     Query Match
Best Local Simi
Matches 101;
                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE 102 amino acid
                                                                                                                                                                                                                                                                                                 TOPOLOGY: line
MOLECULE TYPE: I
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                   FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                             LENGTH: 102 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
TELEX:
                                                        61 STPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 102
                                                                                          78
                                                                                                                                    18 CSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPTNHAVIQTLMNSMDDE 77
                                                                                                                          Н
                                                                                                                                                                                                    Similarity
                                                                                 STPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
                                                                                                                  CSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPTNHAVIQTLMNSMDPE 60
                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                NO Peptide
                                                                                                                                                                                                                                                                                  C-terminal
                                                                                                                                                                                                    86.1%;
99.0%;
                                                                                                                                                                                    0;
                                                                                                                                                                                  Score 559; DB 1; Length 102; Pred. No. 4.3e-55; 0; Mismatches 1; Indels
                                                                                                                                                                                 Indels
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0;

Gaps

0;